

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:18:45 ; Search time 36 Seconds  
(without alignments)  
142.663 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491

Sequence: 1 VAETPTYPWDAETGERLVC.....RVARMGLERSVREPLVPH 271

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_AA:\*  
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3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*  
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6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep:\*  
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13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1491	100.0	300	10	US-09-896-096A-1
2	1491	100.0	300	10	US-09-894-924-1
3	1491	100.0	300	10	US-09-935-727-2
4	1476.5	99.0	289	10	US-09-877-156-17
5	1469	98.5	300	10	US-09-840-795-2
6	1034	69.3	211	10	US-09-877-156-20
7	841	56.4	153	10	US-09-877-156-2
8	671	45.0	170	10	US-09-935-727-4
9	461	30.9	401	10	US-09-062-113-71
10	442.5	29.7	401	10	US-09-062-113-62
11	440.5	29.5	272	10	US-09-062-113-75
12	440.5	29.5	293	10	US-09-896-096A-18
13	440.5	29.5	293	10	US-09-894-924-18
14	440.5	29.5	321	10	US-09-062-113-80
15	440.5	29.5	327	10	US-09-062-113-72
16	440.5	29.5	351	10	US-09-062-113-74
17	440.5	29.5	362	10	US-09-062-113-11
18	440.5	29.5	380	10	US-09-062-113-4
19	440.5	29.5	391	10	US-09-062-113-106

20	440.5	29.5	393	10	US-09-062-113-79	Sequence 79, Appl
21	440.5	29.5	399	10	US-09-062-113-73	Sequence 73, Appl
22	440.5	29.5	401	10	US-09-062-113-5	Sequence 5, Appl
23	440.5	29.5	401	10	US-09-062-113-64	Sequence 64, Appl
24	440.5	29.5	401	10	US-09-062-113-65	Sequence 65, Appl
25	440.5	29.5	401	10	US-09-062-113-66	Sequence 66, Appl
26	440.5	29.5	401	12	US-10-039-785-5	Sequence 5, Appl
27	440.5	29.5	401	12	US-10-066-209-1	Sequence 1, Appl
28	440.5	29.5	401	12	US-10-164-592-2	Sequence 2, Appl
29	433.5	29.1	401	10	US-09-062-113-63	Sequence 63, Appl
30	433	29.0	187	10	US-09-062-113-81	Sequence 81, Appl
31	433	29.0	187	10	US-09-840-795-11	Sequence 11, Appl
32	433	29.0	197	10	US-09-062-113-76	Sequence 76, Appl
33	432	29.0	394	10	US-09-062-113-9	Sequence 9, Appl
34	407	27.3	147	9	US-09-756-854-20	Sequence 20, Appl
35	407	27.3	147	9	US-10-041-574-20	Sequence 20, Appl
36	356.5	23.9	360	10	US-09-062-113-67	Sequence 67, Appl
37	342.5	23.0	450	10	US-09-768-779A-3	Sequence 3, Appl
38	342.5	23.0	461	10	US-09-826-212-4	Sequence 4, Appl
39	342.5	23.0	461	10	US-09-896-096A-17	Sequence 17, Appl
40	342.5	23.0	461	10	US-09-894-924-17	Sequence 17, Appl
41	342.5	23.0	461	10	US-09-840-707A-17	Sequence 17, Appl
42	342.5	23.0	461	10	US-09-935-727-6	Sequence 6, Appl
43	340.5	22.8	461	10	US-09-800-909-2	Sequence 2, Appl
44	340.5	22.8	461	10	US-09-758-124-2	Sequence 2, Appl
45	340.5	22.8	461	10	US-09-800-908-3	Sequence 3, Appl

#### ALIGNMENTS

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RESULT 1
US-09-896-096A-1
; Sequence 1, Application US/09896096A
; Patent No. US2002061559A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYONG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 1
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-096A-1
Query Match      100.0%; Score 1491; DB 10; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.8e-107;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 VAETPTYPWDAETGERLVCACGPPGTFVORPCRRBSPPTCGCPPHRYTQFMNYLERCR 60
Db      30 VAETPTYPWDAETGERLVCACGPPGTFVORPCRRBSPPTCGCPPHRYTQFMNYLERCR 89
QY      61 YCNVLGEREEARACHATINRAACRCRTGFFAHAGFLEHASCPGAGVIAPTPSQNTQ 120
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Db 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 149  
QY 121 CQCPGPTGTSASSSSSSQCPHNRCTALGLALNVPGSSSHDTLTCTGTPPLSTRVPGAE 180  
Db 150 CQCPGPTGTSASSSSSSQCPHNRCTALGLALNVPGSSSHDTLTCTGTPPLSTRVPGAE 209  
QY 181 ECRSAVIDFVAFODISIKRLQRLQALEAPEGWGPTPRAGRAALQLKRRRLTELLGAQD 240  
Db 210 ECRSAVIDFVAFODISIKRLQRLQALEAPEGWGPTPRAGRAALQLKRRRLTELLGAQD 269  
QY 241 GALLVRLLOALRVARMFGLERSVRERFLPVH 271  
Db 270 GALLVRLLOALRVARMFGLERSVRERFLPVH 300

RESULT 2  
US-09-894-924-1  
; Sequence 1, Application US/09894924  
; Patent No. US20020065210A1  
; GENERAL INFORMATION:  
; APPLICANT: ASHKENAZI, AVI J  
; APPLICANT: BOTSTEIN, DAVID  
; APPLICANT: DODGE, KELLY H.  
; APPLICANT: GURNEY, AUSTIN L.  
; APPLICANT: KIM, KYUNG JIN  
; APPLICANT: LAWRENCE, DAVID A.  
; APPLICANT: PITTI, ROBERT  
; APPLICANT: ROY, MARGARET A  
; APPLICANT: TUMAS, DANIEL B  
; APPLICANT: WOOD, WILLIAM I.  
; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog  
; FILE REFERENCE: P1134R2 REVISED  
; CURRENT APPLICATION NUMBER: US/09/894,924  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/157,289  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: US 60/059,288  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: US 60/094,640  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 18  
; SEQ ID NO 1  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-894-924-1

Query Match 100.0%; Score 1491; DB 10; Length 300;  
Best Local Similarity 100.0%; Pred. No. 8.8e-107;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VAETPTYPWRDAETGERLVCAQCPGPTFVQRPCRRDSPTTCGCPPRHYTFQWNYLERCR 60  
Db 30 VAETPTYPWRDAETGERLVCAQCPGPTFVQRPCRRDSPTTCGCPPRHYTFQWNYLERCR 89  
QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 120  
Db 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 149  
QY 121 CQCPGPTGTSASSSSSSQCPHNRCTALGLALNVPGSSSHDTLTCTGTPPLSTRVPGAE 180  
Db 150 CQCPGPTGTSASSSSSSQCPHNRCTALGLALNVPGSSSHDTLTCTGTPPLSTRVPGAE 209  
QY 181 ECRSAVIDFVAFODISIKRLQRLQALEAPEGWGPTPRAGRAALQLKRRRLTELLGAQD 240  
Db 210 ECRSAVIDFVAFODISIKRLQRLQALEAPEGWGPTPRAGRAALQLKRRRLTELLGAQD 269  
QY 241 GALLVRLLOALRVARMFGLERSVRERFLPVH 271  
Db 270 GALLVRLLOALRVARMFGLERSVRERFLPVH 300

RESULT 3

US-09-935-727-2  
; Sequence 2, Application US/09935727  
; Patent No. US20020150583A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P2  
; CURRENT APPLICATION NUMBER: US/09/935,727  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/227,598  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: 09/518,931  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/168,235  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 60/146,371  
; PRIOR FILING DATE: 1999-08-02  
; PRIOR APPLICATION NUMBER: 60/131,964  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/131,270  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/124,092  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/121,774  
; PRIOR FILING DATE: 1999-03-04  
; PRIOR APPLICATION NUMBER: 09/006,352  
; PRIOR FILING DATE: 1998-01-13  
; PRIOR APPLICATION NUMBER: 60/035,496  
; PRIOR FILING DATE: 1997-01-14  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-727-2

Query Match 100.0%; Score 1491; DB 10; Length 300;  
Best Local Similarity 100.0%; Pred. No. 8.8e-107;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VAETPTYPWRDAETGERLVCAQCPGPTFVQRPCRRDSPTTCGCPPRHYTFQWNYLERCR 60  
Db 30 VAETPTYPWRDAETGERLVCAQCPGPTFVQRPCRRDSPTTCGCPPRHYTFQWNYLERCR 89  
QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 120  
Db 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPCPGAGVIAPGTPSQNTQ 149  
QY 121 CQCPGPTGTSASSSSSSQCPHNRCTALGLALNVPGSSSHDTLTCTGTPPLSTRVPGAE 180  
Db 150 CQCPGPTGTSASSSSSSQCPHNRCTALGLALNVPGSSSHDTLTCTGTPPLSTRVPGAE 209  
QY 181 ECRSAVIDFVAFODISIKRLQRLQALEAPEGWGPTPRAGRAALQLKRRRLTELLGAQD 240  
Db 210 ECRSAVIDFVAFODISIKRLQRLQALEAPEGWGPTPRAGRAALQLKRRRLTELLGAQD 269  
QY 241 GALLVRLLOALRVARMFGLERSVRERFLPVH 271  
Db 270 GALLVRLLOALRVARMFGLERSVRERFLPVH 300

RESULT 4  
US-09-877-156-17  
; Sequence 17, Application US/09877156  
; Patent No. US20020055625A1  
; GENERAL INFORMATION:  
; APPLICANT: Catherine Tribouley  
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES

FILE REFERENCE: 1408.003/200130.439C1  
CURRENT APPLICATION NUMBER: US/09/877,156  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 09/286,529  
PRIOR FILING DATE: 1998-04-05  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-877-156-17

Query Match 99.0%; Score 1476.5; DB 10; Length 299;  
Best Local Similarity 99.6%; Pred. No. 1,1e-105;  
Matches 270; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYERCR 60  
DB 30 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYERCR 89  
QY 61 YCNVLCGEREERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 120  
DB 90 YCNVLCGEREERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 149  
QY 121 CQCPGPTFSASSSSBQCPHNRCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 180  
DB 150 CQCPGPTFSASSSSBQCPHNRCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 208  
QY 181 ECERAVIDFAFODISIKRLQRLLOALEAPEGWPPTPRAGAAQLKLRRLTELLGAOD 240  
DB 209 ECERAVIDFAFODISIKRLQRLLOALEAPEGWPPTPRAGAAQLKLRRLTELLGAOD 268  
QY 241 GALLVRLLOALRVARMPGLERSVREERLPVH 271  
DB 269 GALLVRLLOALRVARMPGLERSVREERLPVH 299

RESULT 5  
US-09-840-795-2  
Sequence 2, Application US/09840795  
Patent No. US20020143147A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Erin E.  
APPLICANT: Mattson, Jeanine D.  
APPLICANT: Bates, Elizabeth Esther Mary  
APPLICANT: Gorman, Daniel M.  
APPLICANT: Lebecque, Serge J.E.  
TITLE OF INVENTION: Mammalian Genes; Related Reagents  
FILE REFERENCE: SF0818X  
CURRENT APPLICATION NUMBER: US/09/840,795  
CURRENT FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: 09/351,777  
PRIOR FILING DATE: 1999-07-12  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 300  
TYPE: PRT  
ORGANISM: primate  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (79)  
OTHER INFORMATION: Xaa at residue 79 is undetermined.  
US-09-840-795-2

Query Match 98.5%; Score 1469; DB 10; Length 300;  
Best Local Similarity 98.9%; Pred. No. 4.2e-105;  
Matches 266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYERCR 60  
DB 30 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYERCR 89

QY 61 YCNVLCGEREERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 120  
DB 90 YCNVLCGEREERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 149  
QY 121 CQCPGPTFSASSSSBQCPHNRCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 180  
DB 150 CQCPGPTFSASSSSBQCPHNRCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 209  
QY 181 ECERAVIDFAFODISIKRLQRLLOALEAPEGWPPTPRAGAAQLKLRRLTELLGAOD 240  
DB 210 ECERAVIDFAFODISIKRLQRLLOALEAPEGWPPTPRAGAAQLKLRRLTELLGAOD 269  
QY 241 GALLVRLLOALRVARMPGLERSVREERLPVH 271  
DB 270 GALLVRLLOALRVARMPGLERSVREERLPVH 300

RESULT 6  
US-09-877-156-20  
Sequence 20, Application US/09877156  
Patent No. US20020055625A1  
GENERAL INFORMATION:  
APPLICANT: Catherine Tribouley  
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
FILE REFERENCE: 1408.003/200130.439C1  
CURRENT APPLICATION NUMBER: US/09/877,156  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 09/286,529  
PRIOR FILING DATE: 1998-04-05  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 20  
LENGTH: 211  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-877-156-20

Query Match 69.3%; Score 1034; DB 10; Length 211;  
Best Local Similarity 98.9%; Pred. No. 3.9e-72;  
Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYERCR 60  
DB 30 VAETPTVPMWDAETGERLVCAQCPGTFVORPCRRDPTTCGCPPHHYTQFMNLYERCR 89  
QY 61 YCNVLCGEREERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 120  
DB 90 YCNVLCGEREERARACHATNRAACRCRTGFFAHAGFCLHASCPCPGAGVIAPTGPSQNTQ 149  
QY 121 CQCPGPTFSASSSSBQCPHNRCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 180  
DB 150 CQCPGPTFSASSSSBQCPHNRCTALGLALNVPGSSSHDTLCTGCTGFPPLSTRVPGAE 209  
QY 181 E 181  
DB 210 E 210

RESULT 7  
US-09-877-156-2  
Sequence 2, Application US/09877156  
Patent No. US20020055625A1  
GENERAL INFORMATION:  
APPLICANT: Catherine Tribouley  
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
FILE REFERENCE: 1408.003/200130.439C1  
CURRENT APPLICATION NUMBER: US/09/877,156  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 09/286,529  
PRIOR FILING DATE: 1998-04-05  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0





US-09-062-113-71

Query Match	30.9%;	Score 461;	DB 10;	Length 326;
Best Local Similarity	33.1%;	Pred. No. 2.8e-28;		
Matches 94;	Conservative 57;	Mismatches 101;	Indels 32;	Gaps 7

Qy	5	PTTWBPALEETBERLVCAACPGTGVVOPCRDSDPPTGCGPRHYATOFMYVLECRGYNV	64
Db	26	PKYLHYBETSHTOLCCKCPRGYTLKHCHTAKMKMTVCAPCPGDHYTSDMSHSDCLXSP	85
Qy	65	LCGRBEEBARCAHTNRPACRCRGTGFPAHAGFCLEHASCPGAGVIAGPBSONTOCOPC	124
Db	86	VCKSLQYVKDCNMTNHRVCECKEGRYALEIFCLKHRSCEPGFVGADGTPERTATVCKRC	145
Qy	125	PGTFASASSSECOPIRNTALGLMLNVGSSSHPTLCTSCGPFPLSTRVPQ--AECC	182
Db	146	PDGFSNETSSKACRCRKTNCVSFGLLTQGMNTHDNI---CGSNSESTQKCGIDIDLCC	202
Qy	183	ERAVIDPAFODISIKRLQRLLOALEAPBEGMPTPRAGRAALQIKLR-----RLTELL-	236
Db	203	ENSVQRHGHANLTFEQLRSIMESL-----PEKKVGAEDIEKTIACKSPDIKLLS	255
Qy	237	-----GAQDALLVRLLOLRVARNPGLERSVRE-----RFL	268
Db	256	LWRITNGDQD--TLKGLMHALKHSKTTNFKPTVLOSLLKTIIRFL	297

## RESULT 10

Sequence 62, Application US/09062113  
Patent No. US20020051969A1

GENERAL INFORMATION:

APPLICANT: GOTO, Masaaki  
APPLICANT: TSUDA, Eisuke  
APPLICANT: MOCHIZUKI, Shin'ichi  
APPLICANT: YANO, Kazuki  
APPLICANT: KOBAYASHI, Fumie  
APPLICANT: SHIMA, No. US20020051969A1uyuki  
APPLICANT: YASUDA, Hisataka  
APPLICANT: NAKAGAWA, No. US20020051969A1uaki  
APPLICANT: MORINAGA, Tomomori  
APPLICANT: UEDA, Masatsugu  
APPLICANT: HIGASHIO, Kanji  
TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing  
TITLE OF INVENTION: the Proteins  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Teata, Hurwitz & Thibeault  
STREET: 125 High St.  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/062,113  
FILING DATE: 17-APR-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 54977/1995  
FILING DATE: 20-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 207508/1995  
FILING DATE: 21-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/00374  
FILING DATE: 20-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,004

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1      FILING DATE: 20-FEB-1996
2      ATTORNEY/AGENT INFORMATION:
3      NAME: MOORE, Ronda P.
4      REGISTRATION NUMBER: 44,244
5      REFERENCE/DOCKET NUMBER: FJN-060DV
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: (617) 248-7000
8      TELEFAX: (617) 248-7100
9      INFORMATION FOR SEQ ID NO: 62:
10     SEQUENCE CHARACTERISTICS:
11     LENGTH: 401 amino acids
12     TYPE: amino acid
13     STRANDEDNESS:
14     TOPOLOGY: linear
15     MOLECULE TYPE: protein
16     FEATURE:
17     NAME/KEY: Peptide
18     LOCATION: -21..0
19     FEATURE:
20     NAME/KEY: Protein
21     LOCATION: 1..380
22     OTHER INFORMATION: /note= "OC1F-C19S"
23
24 US-09-062-113-62

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US-09-062-113-62

Query Match	29.7%	Score 442.5;	DB 10;	Length 401;
Best Local Similarity	41.2%	Pred. No. 9.1e-27;		
Matches 77; Conservative	31;	Mismatches 74;	Indels 5;	Gaps 2

QY		5	P Y W M R A E G R I V C A Q C P P F V O B P C R D S P T G C P P H H Y O F N U L E C R C N V	64
Db		26	P K I H Y B E F S H Q L C D K C P G T Y L K H C T A K K T V A P C P D H Y T D S W H T S D C L Y C S P	85
QY		65	L G G R E E B A R C H A T H R R A C R C R G T F F A H G C L E H A S C P G A G V I A P G T P S O N T O C P C	124
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QY		125	P G G T S A S S S S E D C C O P R R C T A L G L A I N P G S S H D T L T C T G F L S T R V G A E --C	182
Db		146	P D G F S N E T S S K A P R C R H T N C S V F G L L T O K N A T H N I ---C S G N S E S T O K S G I D V T L C	202
QY		183	E R A Y I D F	189
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## RESULT 11

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US-09-062-113-75
; Sequence 75, Application US/09062113
; Patent No. US20020051969A1
;
GENERAL INFORMATION:
;
APPLICANT: GOTO, Masaaki
APPLICANT: TSUDA, Eisuke
APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: KOBAYASHI, Fumie
APPLICANT: SHIMA, No. US20020051969A1yuki
APPLICANT: YASUDA, Hisataka
APPLICANT: NAKAGAWA, No. US20020051969A1uaki
APPLICANT: MORINAGA, Tomonori
APPLICANT: UEDA, Maatsugu
APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969A1e1 Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/062,113  
FILING DATE: 17-APR-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 54977/1995  
FILING DATE: 20-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 207508/1995  
FILING DATE: 21-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/00374  
FILING DATE: 20-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,004  
FILING DATE: 20-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MOORE, Ronda P.  
REGISTRATION NUMBER: 44,244  
REFERENCE/DOCKET NUMBER: FJN-060DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 272 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: -21..0  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..251  
OTHER INFORMATION: /note= "OCIF-CDD2"  
US-09-062-113-75

Query Match 29.5%; Score 440.5; DB 10; Length 272;  
Best Local Similarity 41.2%; Pred. No. 8.5e-27;  
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;  
  
QY 5 PTPWRDAETGERLVCAQCPGTFVORPCRRDSPPTCGPCPPRHVYQFWNYLRCRYCNV 64  
Db 26 PKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSP 85  
  
QY 65 LCGREERAEARACHATHNRACRGTGFFAHAGFCLEHASCPGAGVIAFGTPSQNTQOCPC 124  
Db 86 VKELQVVKQECNTRNVRVCEKGRYLEIEFCLKHRSPPGPGVQAGTPERTVTKRC 145  
  
QY 125 PPGTFSSSSSSQCPHRNCTALGLALNVGSSSHDTLTCTSGTGPLSTRVPGAEE--C 182  
Db 146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC 202  
  
QY 183 ERAVIDF 189  
Db 203 EEAFFRF 209  
  
RESULT 12  
US-09-896-096A-18  
; Sequence 18, Application US/09896096A  
; Patent No. US20020061559A1  
; GENERAL INFORMATION:  
; APPLICANT: ASHKENAZI, AVI J  
; APPLICANT: BOTSTEIN, DAVID  
; APPLICANT: DODGE, KELLY H.  
; APPLICANT: GURNEY, AUSTIN L.  
; APPLICANT: KIM, KYUNG JIN  
; APPLICANT: LAWRENCE, DAVID A.  
; APPLICANT: PITTI, ROBERT  
; APPLICANT: ROY, MARGARET A  
; APPLICANT: TUMAS, DANIEL B  
; APPLICANT: WOOD, WILLIAM I.  
; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog  
; FILE REFERENCE: P1134R2 REVISED  
; CURRENT APPLICATION NUMBER: US/09/894,924  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/157,289  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: US 60/059,288  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: US 60/094,640  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 18  
; SEQ ID NO 18  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens

APPLICANT: LAWRENCE, DAVID A.  
APPLICANT: PITTI, ROBERT  
APPLICANT: ROY, MARGARET A  
APPLICANT: TUMAS, DANIEL B  
APPLICANT: WOOD, WILLIAM I.  
TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog  
FILE REFERENCE: P1134R2 REVISED  
CURRENT APPLICATION NUMBER: US/09/896,096A  
CURRENT FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: US 09/157,289  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: US 60/059,288  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: US 60/094,640  
PRIOR FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 18  
SEQ ID NO 18  
LENGTH: 293  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-896-096A-18  
  
Query Match 29.5%; Score 440.5; DB 10; Length 293;  
Best Local Similarity 41.2%; Pred. No. 9.2e-27;  
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;  
  
QY 5 PTPWRDAETGERLVCAQCPGTFVORPCRRDSPPTCGPCPPRHVYQFWNYLRCRYCNV 64  
Db 26 PKYLHYDEETSHQLLCKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECLYCSP 85  
  
QY 65 LCGREERAEARACHATHNRACRGTGFFAHAGFCLEHASCPGAGVIAFGTPSQNTQOCPC 124  
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QY 183 ERAVIDF 189  
Db 203 EEAFFRF 209  
  
RESULT 13  
US-09-894-924-18  
; Sequence 18, Application US/09894924  
; Patent No. US20020065210A1  
; GENERAL INFORMATION:  
; APPLICANT: ASHKENAZI, AVI J  
; APPLICANT: BOTSTEIN, DAVID  
; APPLICANT: DODGE, KELLY H.  
; APPLICANT: GURNEY, AUSTIN L.  
; APPLICANT: KIM, KYUNG JIN  
; APPLICANT: LAWRENCE, DAVID A.  
; APPLICANT: PITTI, ROBERT  
; APPLICANT: ROY, MARGARET A  
; APPLICANT: TUMAS, DANIEL B  
; APPLICANT: WOOD, WILLIAM I.  
; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog  
; FILE REFERENCE: P1134R2 REVISED  
; CURRENT APPLICATION NUMBER: US/09/894,924  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/157,289  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: US 60/059,288  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: US 60/094,640  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 18  
; SEQ ID NO 18  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-894-924-18

Query Match	29.5%;	Score 440.5;	DB 10;	Length 293;
Best Local Similarity	41.2%;	Pred. No. 9.2e-27;		
Matches 77;	Conservative 31;	Mismatches 74;	Indels 5;	Gaps 2;

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      26  PKYLHYDEBTSHQLCDKCPRGTYLKHQCTAKMKITVACPCGDHYTDSWHTSDECLYCSP 85
QY      65  LCGEREERARACHATHNACRCRTGFFAHAGFCLEHAACPPAGVIAAGTSPONTQOPC 124
      86  VCKEQAYVQKQECNTRHNVCCECKEGRYLEIFCLCKHSCPPGFGVQAGTPEBRTVCKRC 145
QY      125  PPGTFSSASSSSBOCQPHRNNTALGLALNVGSSSHDTLCTSCGFLSTRVPAEE--C 182
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Db      183  ERAVIDF 189
      203  EEAFFRF 209
Db

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RESULT 14  
US-09-062-113-80

APPLICANT: GOTO, Masaaki  
 APPLICANT: TSUDA, Eisuke  
 APPLICANT: MOCHIZUKI, Shin'ichi  
 APPLICANT: YANO, Kazuki  
 APPLICANT: KOBAYASHI, Fumie  
 APPLICANT: SHIMA, No. US20020051969A1uyuki  
 APPLICANT: YASUDA, Hisataka  
 APPLICANT: NAKAGAWA, No. US20020051969A1uaki  
 APPLICANT: MORINAGA, Tomonori  
 APPLICANT: UEDA, Masateugu  
 APPLICANT: HIGASHIO, Kanji  
 TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing  
 TITLE OF INVENTION: the Proteins  
 NUMBER OF SEQUENCES: 108  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Teeta, Hurwitz & Thibault  
 STREET: 125 High St.

REFERENCE/DOCKET NUMBER: FJN-060DVA  
TELECOMMUNICATION INFORMATION:

OTHER INFORMATION: /note= "OCIF-CSph"  
US-09-062-113-80

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QY      5 PTYMRDLDETERLVCAACCPGTVVSPRCRSDSPTCGCPCHRYTGFQWNLIEGRCYCNV 64
Dh      26 PKYLHYDEETISHQLCDKCPGPTYLKHQCTAKMKTVCAPCPDHYTDSWHTSDCLYCSP 85

QY      65 LCGREEBEABACHATNHRACRRTGFPMAHGCLEHASCPGAGVIAGPSPONTQOCPC 124
Dh      86 VCKELQYVKGCCNKRTHNRVCECKRGRLYEIEFLKAHRSCPPGFEVQAQGTERTNTVCKRC 145

QY      125 PPGTFSASSSSSECCOPHRNCTALGLALNPGSSSHDTLCTGCTGFPULSTRVGAEE--C 182
Dh      146 PDGFSNETHSKAPCRKHNCISVFGLLTLQKGNATHDNI---CSGNSSESTOKCSDIVTLIC 202

QY      183 ERAVIDF 189
Dh      203 EEAFFRF 209

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RESULT 15  
US-09-062-113-72

1 APPLICANT: GOTO, Masaaki  
 2 APPLICANT: TSUDA, Eisuke  
 3 APPLICANT: MOCHIZUKI, Shin'ichi  
 4 APPLICANT: YANO, Kazuki  
 5 APPLICANT: KOBAYASHI, Fumie  
 6 APPLICANT: SHIMA, No. US20020051969A1uyuki  
 7 APPLICANT: YASUDA, Hisataka  
 8 APPLICANT: NAKAGAWA, No. US20020051969A1uaki  
 9 APPLICANT: MORINAGA, Tomonori  
 10 APPLICANT: UEDA, Masatsugu  
 11 APPLICANT: HIGASHIO, Kanji  
 12 TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing  
 13 TITLE OF INVENTION: the Proteins  
 14 NUMBER OF SEQUENCES: 108  
 15 CORRESPONDENCE ADDRESS:  
 16 ADDRESSEE: Testa, Hurwitz & Thibault  
 17 STREET: 125 High St.  
 18 CITY: Boston  
 19 STATE: MA  
 20 COUNTRY: USA  
 21 ZIP: 02110  
 22 COMPUTER READABLE FORM:  
 23 MEDIUM TYPE: Floppy disk  
 24 COMPUTER: IBM PC compatible  
 25 OPERATING SYSTEM: PC-DOS/MS-DOS  
 26 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 27 CURRENT APPLICATION DATA:

Search completed: January 6, 2003, 11:27:02  
Job time : 37 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:31 ; Search time 61 Seconds

(without alignments)  
591.982 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1491	100.0	271	20	AAV42184	Human mFLINT #1 pr
2	1491	100.0	271	21	AA19334	A mature human FAS
3	1491	100.0	271	21	AA19705	Human FAS ligand 1
4	1491	100.0	271	21	AAV97247	M68 TNF receptor r
5	1491	100.0	271	21	AAV96598	Human mature FLINT
6	1491	100.0	271	22	AA803567	Human mature fas l
7	1491	100.0	271	22	AA868044	Amino acid sequenc
8	1491	100.0	271	22	AA868047	Amino acid sequenc
9	1491	100.0	271	22	AA874465	Human FLINT mature
10	1491	100.0	271	23	AAE14578	Human mature FLINT

11	1491	100.0	300	19	AAW66102	Amino acid sequenc
12	1491	100.0	300	19	AAW63622	Human tumour necro
13	1491	100.0	300	20	AAV03099	Human lung TNF-rec
14	1491	100.0	300	20	AAV42182	Human FLINT #1 pro
15	1491	100.0	300	20	AAV17479	Mammalian tumour n
16	1491	100.0	300	20	AAV06817	Human DCR3 polypep
17	1491	100.0	300	20	AAW97749	Human tumour necro
18	1491	100.0	300	20	AAW95082	Orphan receptor (H
19	1491	100.0	300	21	AA19335	A full length huma
20	1491	100.0	300	21	AA826559	Human soluble TNF
21	1491	100.0	300	21	AA824057	Human PRO212 prote
22	1491	100.0	300	21	AA833416	Human PRO212 prote
23	1491	100.0	300	21	AA803621	Human Fas ligand 1
24	1491	100.0	300	21	AAV97246	M68 TNF receptor r
25	1491	100.0	300	21	AAV90357	Human tumour necro
26	1491	100.0	300	21	AA824395	Human PRO212 prote
27	1491	100.0	300	21	AAV96596	Human FLINT. Homo
28	1491	100.0	300	22	AAE03568	Human native fas l
29	1491	100.0	300	22	AA874466	Human FLINT native
30	1491	100.0	300	22	AA871754	Human NTR3. Homo
31	1491	100.0	300	22	AA848161	Human PRO212 polyp
32	1491	100.0	300	22	AA850903	Human PRO212 prote
33	1491	100.0	300	23	AAE14579	Human native FLINT
34	1491	100.0	300	23	AAE20848	Human tumour necro
35	1491	100.0	341	22	AA873740	Human colon cancer
36	1487	99.7	271	21	AA819709	Protease-resistant
37	1487	99.7	271	21	AA803571	Human mature fas l
38	1487	99.7	271	22	AA874467	Human FLINT mature
39	1487	99.7	271	23	AAE14581	Human protease-res
40	1486	99.7	271	23	AAE03584	Human mature fas l
41	1486	99.7	271	23	AAE14582	Human protease-res
42	1485	99.6	271	21	AAV96599	Human mature FLINT
43	1485	99.6	271	23	AAE14583	Human protease-res
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45	1485	99.6	271	23	AAE14586	Human protease-res

#### ALIGNMENTS

RESULT 1	
AAV42184	
ID	AAV42184 standard; Protein; 271 AA.
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AC	AAV42184.
XX	
DT	17-DEC-1999 (first entry)
XX	
DE	Human mFLINT #1 protein sequence.
XX	
KW	Human; FLINT; mFLINT; OPB3; tumour necrosis factor receptor; FasL;
KW	apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW	sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW	refusion-associated injury; aplastic anaemia; differentiation;
KW	growth; myelodysplastic syndrome; pancytopenic condition;
KW	myocardial ischaemia.
XX	
OS	Homo sapiens.
XX	
PN	WO950413-A2.
XX	
PD	07-OCT-1999.
XX	
PF	30-MAR-1999; 99WO-US06797.
XX	
PR	30-MAR-1998; 98US-0079856.
XX	
PR	20-MAY-1998; 98US-0086074.
XX	
PR	09-SEP-1998; 98US-0096433.
XX	
PR	17-DEC-1998; 98US-0112577.
XX	
PR	18-DEC-1998; 98US-0112703.
XX	
PR	18-DEC-1998; 98US-0112933.
XX	
PR	22-DEC-1998; 98US-0113407.
XX	

PA (ELIL ) LILLY & CO ELI.  
XX Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;  
PI Hui KY, Khaitonenkov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;  
XX Song HY, Wang J, Wu X, Zuckerman SH;  
XX WPI: 1999-591319/50.  
DR N-PSDB; AA225377.  
XX  
PT Use of mature FLINT for treating acute liver failure, inflammation,  
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic  
PT and proinflammatory activity  
XX  
PS Claim 31; Fig 3; 99pp; English.  
XX  
CC The present invention describes therapeutic applications of mature FLINT  
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT  
CC (mFLINT), which is a member of the tumour necrosis factor receptor  
CC superfamily, is used for treating acute liver failure, inflammation of  
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated  
CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated  
CC injury or disorder such as hypercoagulation (including use with  
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury  
CC or disorder. Type I diabetes, cancer, cell damage or damage to an  
CC innocent bystander tissue that is induced by a chemotherapeutic agent or  
CC therapeutic irradiation, treating haematopoietic progenitor cells that  
CC have been exposed to therapeutic radiation or chemotherapy, aplastic  
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is  
CC also used for promoting the growth or differentiation of a haematopoietic  
CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte  
CC resulting from abnormal myocardial ischaemia. The present sequence  
CC represents human mFLINT.  
XX  
SQ Sequence 271 AA;  
Query Match 100.0%; Score 1491; DB 20; Length 271;  
Best Local Similarity 100.0%; Pred No. 8.5e-115;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 VAETPTYPWRDAETGERLVCAQCPGGTFVQRPCRRDSPTTCGPPRRHYTQFWNYLERCR 60  
QY 61 YCNVLGEREEERACHATNCRACRGTGFPAHAGFLEHASCPGAGVAPGTPSNTQ 120  
Db 61 YCNVLGEREEERACHATNCRACRGTGFPAHAGFLEHASCPGAGVAPGTPSNTQ 120  
QY 121 CQCPGCTFSASSSSSQCPHNRCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGA 180  
Db 121 CQCPGCTFSASSSSSQCPHNRCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGA 180  
QY 181 ECERAVIDFAVDISIKRLQRLQALEAPEGMGPTPRAGRAALQLKRRRLTELLGAQD 240  
Db 181 ECERAVIDFAVDISIKRLQRLQALEAPEGMGPTPRAGRAALQLKRRRLTELLGAQD 240  
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Db 241 GALLVRLQLALRVARMPLGLRSVRERFLPVH 271  
RESULT 2  
AAB19334  
ID AAB19334 standard; Protein; 271 AA.  
XX  
AC AAB19334;  
XX  
DT 19-FEB-2001 (first entry)  
XX  
DE A mature human FAS Ligand Inhibitory Protein (FLINT).  
XX  
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;  
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;  
KW acute respiratory distress syndrome; ulcerative colitis;

KW chronic obstructive pulmonary disease; Crohn's disease.  
XX  
OS Homo sapiens.  
PH Key Location/Qualifiers  
FT Misc-difference 1 /note= "optionally replaced with Met"  
FT Misc-difference 2 /note= "optionally replaced with Asn"  
FT Misc-difference 4 /note= "optionally replaced with Ala"  
FT Misc-difference 12 /note= "optionally replaced with Asn"  
FT Misc-difference 13 /note= "optionally replaced with Asp or Gln"  
FT Misc-difference 17 /note= "optionally replaced with Trp"  
FT Misc-difference 25 /note= "optionally replaced with Asn"  
FT Misc-difference 34 /note= "optionally replaced with Asn"  
FT Misc-difference 35 /note= "optionally replaced with Asn"  
FT Misc-difference 36 /note= "optionally replaced with Thr"  
FT Misc-difference 37 /note= "optionally replaced with Asn or Thr"  
FT Misc-difference 38 /note= "optionally replaced with Asn"  
FT Misc-difference 53 /note= "optionally replaced with Asp"  
FT Misc-difference 63 /note= "optionally replaced with Trp"  
FT Misc-difference 67 /note= "optionally replaced with Asp"  
FT Misc-difference 69 /note= "optionally replaced with Glu"  
FT Misc-difference 75 /note= "optionally replaced with Pro"  
FT Misc-difference 82 /note= "optionally replaced with Glu or Thr"  
FT Misc-difference 88 /note= "optionally replaced with Pro"  
FT Misc-difference 94 /note= "optionally replaced with Tyr"  
FT Misc-difference 95 /note= "optionally replaced with Asp"  
FT Misc-difference 96 /note= "optionally replaced with Gln"  
FT Misc-difference 101 /note= "optionally replaced with Thr"  
FT Misc-difference 102 /note= "optionally replaced with Leu"  
FT Misc-difference 104 /note= "optionally replaced with Ser"  
FT Misc-difference 107 /note= "optionally replaced with Ser, Asp, Glu or Thr"  
FT Misc-difference 110 /note= "optionally replaced with Met, Thr or Glu"  
FT Misc-difference 114 /note= "optionally replaced with Asn"  
FT Misc-difference 115 /note= "optionally replaced with Asn"  
FT Misc-difference 126 /note= "optionally replaced with Asn"  
FT Misc-difference 132 /note= "optionally replaced with Asn"  
FT Misc-difference 134 /note= "optionally replaced with Thr"  
FT Misc-difference 162 /note= "optionally replaced with Ala"  
FT Misc-difference 166 /note= "optionally replaced with Asn"  
FT

```

FT      Misc-difference 169 /note= "optionally replaced with Ala"
FT      Misc-difference 171 /note= "optionally replaced with Asn"
FT      Misc-difference 172 /note= "optionally replaced with Asn"
FT      Misc-difference 179 /note= "optionally replaced with Thr"
FT      Misc-difference 183 /note= "optionally replaced with Lys"
FT      Misc-difference 194 /note= "optionally replaced with Asn"
FT      Misc-difference 196 /note= "optionally replaced with Thr"
FT      Misc-difference 209 /note= "optionally replaced with Thr"
FT      Misc-difference 225 /note= "optionally replaced with Thr"
FT      Misc-difference 237 /note= "optionally replaced with Arg"
FT      Misc-difference 270 /note= "optionally replaced with Glu"
FT      Misc-difference 270 /note= "optionally replaced with Gly"
XX
PN      WO200058465-A2.
XX
XX      05-OCT-2000.
XX
XX      20-MAR-2000; 2000WO-US06417.
XX
XX      30-MAR-1999; 99US-0126839.
XX      21-JUN-1999; 99US-0140077.
XX      21-JUN-1999; 99US-0140156.
XX      20-OCT-1999; 99US-0160566.
XX      18-FEB-2000; 2000US-0183398.
XX
XX      (EIL) Lilly & CO ELI.
XX
XX      Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micancovic R;
XX      Newton CM, Nobilit TW, Rathmachalam R, Techar SR, Witcher DR,
XX      Wroblewski VJ;
XX      WPI; 2000-656167/63.
XX      N-PSDB; AAA75999.
XX
XX      FAS ligand inhibitory Protein analogs useful for treating abnormal
XX      apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,
XX      chronic obstructive pulmonary disease ulcerative colitis or Crohn's
XX      disease -
XX
XX      Claim 1; Page 112-113; 114pp; English.
XX
XX      The present sequence represents a mature human FAS ligand inhibitory
XX      protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor
XX      proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature
XX      FLINT protein is modified to produce analogues, which have greater
XX      potency, longer in vivo half-lives, decreased aggregation, decreased
XX      absorption onto surfaces, increased solubility and improved ease of
XX      formulation. The FLINT analogue is useful for treating a patient
XX      suffering from disease or condition relating to abnormal apoptosis such
XX      as acute lung injury, acute respiratory distress syndrome, pulmonary
XX      fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or
XX      Crohn's disease.
XX
XX      Sequence 271 AA;
XX

```

Query Match	100.0%	Score 1491, DB 21,	Length 271,
Best Local Similarity	100.0%	Pred. No. 8.Se-115;	
Matches 271; Conservative	0;	Mismatches	0; Gaps 0;

QY 1 VAEPTTYWMDAETGERLVCAQCPGTFVQRPCCRDSPPTCGCPRRHYTQFNNYLER 60

Db 1 VAEPTTYWMDAETGERLVCAQCPGTFVQRPCCRDSPPTCGCPRRHYTQFNNYLER 60

QY	61	YCNVLCGRREBEAACHATNHRACRCRTGPPAHAGFCLBHASCPPGAGVLA	AGPTGSPQNTQ	120
Db	61	YCNVLCGRREBEAACHATNHRACRCRTGPPAHAGFCLBHASCPPGAGVLA	AGPTGSPQNTQ	120
QY	121	CQPCPGTFSASSSSSBOCCPHRCNCTALGLALNVPGSSSHDTLCTCTG	FPPLSTRVGAE	180
Db	121	CQPCPGTFSASSSSSBOCCPHRCNCTALGLALNVPGSSSHDTLCTCTG	FPPLSTRVGAE	180
QY	181	ECERAVIDFVAFODISIKRLQRLQALEAPBEGWGPTRAGAAQLKLRRRL	TELLGAQD	240
Db	181	ECERAVIDFVAFODISIKRLQRLQALEAPBEGWGPTRAGAAQLKLRRRL	TELLGAQD	240
QY	241	GALLVRLQLALRVARMPGLERSVERELPYN	271	
Db	241	GALLVRLQLALRVARMPGLERSVERELPYN	271	

RESULT 3
AAB19705
ID AAB19705 standard; Protein; 271 AA

AA  
AC      AAB19705;

DT 05-FEB-2001 (first entry)

Human FAS ligand inhibitor protein FLINT.

KM ELINT; FAS ligand inhibitory protein; human; protease resistant.  
KM acute lung injury; acute respiratory distress syndrome;  
KM chronic obstructive pulmonary disease; pulmonary fibrosis;  
KM ulcerative colitis; therapy; organ transplantation.

yy Homo sapiens.

	Key	Location/Qualifiers
FH		
FT	Cleavage-site	218, 219

FT	/note= "cleaved by trypsin-like proteases"
FT	
Misc-difference	
FT	34

/note= "optionally replaced by Arg, as given in Claims 10, 11, 13 and 14"

FT	Misc-difference	36
FT	/note=	"optionally replaced by Thr, as given in

FT	Misc-difference 132	Claims 10, 11, 13 and 14"
FT		

FT /note= "optionally replaced by Asn, as given in  
ET Claim 12"

FT	Misc-difference	194	/note= "optionally replaced by Asn, as given in
FT			

FT	Claims 11 and 14"
FT	
Misc-difference 196	

/note= "optionally replaced by Thr, as given in Claims 11 and 14"

FT	Misc-difference	214
FT	/note=	"optionally replaced by any naturally

ET	occurring amino acid"
ET	
Misc-difference	215
ET	

/note= "optionally replaced by any naturally occurring amino acid"

FT	Misc-difference	216	/note= "optionally replaced by any naturally
FT			

occurring amino acid, preferably pro as given in Claims 9 and 15"

FT	Misc-difference	217	/note= "optionally replaced by any naturally
FT			

FT occurring amino acid, preferably tyr as  
FT given in Claim 9"

FT	Misc-difference	218	/note= "optionally replaced by any naturally
FT			

FT occurring amino acid, preferably Gln, G  
Ala, Gly, Ser, Val, Tyr or Asn as given

FT Claims, 9, 10, 11, 12, especially 31 and 32 given in Claims 13, 14, 15, 35 and 36"

FI Misc-Allference 219





CC apoptosis including systemic lupus erythematosus, Hashimoto's  
 CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune  
 CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,  
 CC liver diseases, autoimmune gastritis, ulcerative colitis,  
 CC glomerulonephritis, pulmonary fibrosis, heart failure,  
 CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,  
 CC osteoporosis, Alzheimer's disease, Parkinson's disease, stroke, and  
 CC myocardial infarction.

XX Sequence 271 AA:

Query Match 100.0%; Score 1491; DB 21; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTPYPMWDAETGERLVCACQCPGTFVQPCGRDPTTCGCPPHRYTOFNNYLERCR 60  
 DB 1 VAETPTYPWMDAETGERLVCACQCPGTFVQPCGRDPTTCGCPPHRYTOFNNYLERCR 60

QY 61 YCNVLGGEREEEARACHATNRAACRCRTGFFAHAGFCLHASCPPGAGVIAPTGPSQNTQ 120  
 DB 61 YCNVLGGEREEEARACHATNRAACRCRTGFFAHAGFCLHASCPPGAGVIAPTGPSQNTQ 120

QY 121 COPCPGTFSSASSSSSEOCOPHNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAE 180  
 DB 121 COPCPGTFSSASSSSSEOCOPHNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAE 180

QY 181 ECERAVIDFAFODISIKRLQRLQALEAPBEGMPTPRAGRAALQKLRRRLTELLGAOD 240  
 DB 181 ECERAVIDFAFODISIKRLQRLQALEAPBEGMPTPRAGRAALQKLRRRLTELLGAOD 240

QY 241 GALLVRLQALRVARNMPGLERSVREERFLPVH 271  
 DB 241 GALLVRLQALRVARNMPGLERSVREERFLPVH 271

RESULT 5  
 AAY96598  
 ID AAY96598 standard; Protein; 271 AA.

AC AAY96598;  
 DT 26-SEP-2000 (first entry)  
 DE Human mature FLINT.  
 DE Human mature FLINT.  
 KM FLINT; osteoprotegerin 3, OPG3; tumour necrosis factor receptor; TNFR,  
 KM FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotrophic;  
 KM anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cycostatic;  
 KM anti-inflammatory; antibacterial; immunosuppressive.

OS Homo sapiens.  
 PN WO200037094-A2.  
 PD 29-JUN-2000.  
 PF 21-DEC-1999; 99WO-US30734.  
 PR 22-DEC-1998; 98US-0113407.  
 PR 30-MAR-1999; 99WO-US06797.  
 PR 20-OCT-1999; 99US-0172239.  
 PA (ELIL ) LILLY & CO ELI.  
 PI Cohen FU, Posada JA, Wierda D;  
 DR WPI; 2000-475441/41.  
 DR N-PSDB; AAA51077.  
 PT Use of mature FLINT for treating e.g. acute respiratory distress  
 PT syndrome, ulcerative colitis or ischemic injury during organ  
 PT transplantation

XX Example 8; Fig 3; 125pp; English.

PS Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis  
 XX factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and  
 CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas  
 CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for  
 CC treating acute respiratory distress syndrome, treating or inhibiting  
 CC ulcerative colitis, inhibiting ischemic injury during organ  
 CC transplantation or for organ preservation during transplantation. mFLINT  
 CC can also be used to treat acute liver failure, inflammation of the liver,  
 CC abnormal (hepatocyte) apoptosis, sepsis, disorders associated with  
 CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,  
 CC damage to a cardiac myocyte resulting from abnormal myocardial ischemia,  
 CC Type I diabetes, cancer, damage to an innocent bystander tissue induced  
 CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,  
 CC myelodysplastic syndromes and pancytopenic conditions.

XX Sequence 271 AA:

Query Match 100.0%; Score 1491; DB 21; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 8.5e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTPYPMWDAETGERLVCACQCPGTFVQPCGRDPTTCGCPPHRYTOFNNYLERCR 60  
 DB 1 VAETPTYPWMDAETGERLVCACQCPGTFVQPCGRDPTTCGCPPHRYTOFNNYLERCR 60

QY 61 YCNVLGGEREEEARACHATNRAACRCRTGFFAHAGFCLHASCPPGAGVIAPTGPSQNTQ 120  
 DB 61 YCNVLGGEREEEARACHATNRAACRCRTGFFAHAGFCLHASCPPGAGVIAPTGPSQNTQ 120

QY 121 COPCPGTFSSASSSSSEOCOPHNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAE 180  
 DB 121 COPCPGTFSSASSSSSEOCOPHNCTALGLALNVGSSSHDTLCTSCGFPPLSTRVPGAE 180

QY 181 ECERAVIDFAFODISIKRLQRLQALEAPBEGMPTPRAGRAALQKLRRRLTELLGAOD 240  
 DB 181 ECERAVIDFAFODISIKRLQRLQALEAPBEGMPTPRAGRAALQKLRRRLTELLGAOD 240

QY 241 GALLVRLQALRVARNMPGLERSVREERFLPVH 271  
 DB 241 GALLVRLQALRVARNMPGLERSVREERFLPVH 271

RESULT 6  
 AAE03567  
 ID AAE03567 standard; Protein; 271 AA.

AC AAE03567;  
 DT 04-AUG-2001 (first entry)  
 DE Human mature fas ligand inhibitory protein (FLINT).  
 DE Human mature fas ligand inhibitory protein (FLINT).  
 KM Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;  
 KM TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;  
 KM acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;  
 KM chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;  
 KM rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;  
 KM fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;  
 KM chronic renal failure; graft-vs-host disease; cutaneous inflammation;  
 KM vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;  
 KM insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;  
 KM Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;  
 KM Down's syndrome; multiple sclerosis; cycostatic; neurotropic;  
 KM neuroprotective; vasotrophic.

OS Homo sapiens.  
 PN AAE03567  
 PD 04-AUG-2001 (first entry)  
 PF Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;  
 PR TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;  
 PR acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;  
 PR chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;  
 PR rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;  
 PR fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;  
 PR chronic renal failure; graft-vs-host disease; cutaneous inflammation;  
 PR vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;  
 PR insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;  
 PR Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;  
 PR Down's syndrome; multiple sclerosis; cycostatic; neurotropic;  
 PR neuroprotective; vasotrophic.

Key Location/Qualifiers  
 Modified-site 144  
 /note= "N-linked glycosylation site"

FT Modified-site 174 /note= "O-linked glycosylation site"  
FT FT 216  
FT Modified-site /note= "O-linked glycosylation site"  
FT FT 218..219  
FT Cleavage-site /note= "Proteolytic cleavage"  
XX XX  
XX WO200142463-A1.  
XX XX  
XX 14-JUN-2001.  
XX XX  
XX 29-NOV-2000; 2000WO-US30166.  
XX XX  
XX 07-DEC-1999; 99US-0169367.  
XX PR 07-DEC-1999; 99US-0169381.  
XX PR 07-DEC-1999; 99US-0169412.  
XX PR 23-MAR-2000; 2000US-0191430.  
XX XX  
XX (ELIL ) LILLY & CO ELI.  
XX PA  
XX Lu J, Witcher DR;  
XX PI  
XX XX  
XX WPI; 2001-381684/40.  
XX DR N-PSDE; AAD07380.  
XX DR

XX New FLINT polypeptide for treating and/or preventing acute lung injury,  
XX acute respiratory distress syndrome, ulcerative colitis, and  
XX graft-versus-host disease, comprises O-linked or N-linked  
XX oligosaccharides -

XX Example 1; Page 52-53; 60pp; English.

XX The present sequence is human mature fas ligand inhibitory protein  
XX (FLINT). FLINT, a homologue of tumour necrosis factor receptor  
XX protein (TNFR), binds fas ligand (FasL) and thereby preventing the  
XX interaction of FasL with fas. FLINT comprising O-linked or N-linked  
XX oligosaccharides is useful for preventing or treating acute lung injury  
XX (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,  
XX chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),  
XX to facilitate organ preservation for transplantation and to inhibit T  
XX lymphocyte activation. FLINT is useful for treating and/or preventing  
XX diseases such as rheumatoid arthritis, fibroproliferative lung disease,  
XX fibrotic lung disease, acute lung injury, human immunodeficiency virus  
XX (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-  
XX host disease, cutaneous inflammation, vascular leak syndrome,  
XX Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent  
XX diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease, such as  
XX Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease, such as  
XX psoriasis, Down's syndrome, and multiple sclerosis.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;  
Best Local Similarity 100.0%; Pred. No. 8.5e-115; Indels 0; Gaps 0;  
Matches 271; Conservative 0; Mismatches 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 60  
DB 1 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 60  
QY 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120  
DB 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120  
QY 121 CQCPPGTFSASSSSSQCPHRNCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180  
DB 121 CQCPPGTFSASSSSSQCPHRNCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180  
QY 181 ECERAVIDFVAFQDISIKRLQRLLOALEAPEGWGTPPRAGRAALQLKLRRLTELLGAQD 240  
DB 181 ECERAVIDFVAFQDISIKRLQRLLOALEAPEGWGTPPRAGRAALQLKLRRLTELLGAQD 240  
QY 241 GALLVRLLOALRVARMPLGLERSVRERFLPVH 271

DB 241 GALLVRLLOALRVARMPLGLERSVRERFLPVH 271

RESULT 7

ID AAB68044  
AC AAB68044;

DT 29-JUN-2001 (first entry)

DE Amino acid sequence of a human mature FLINT polypeptide.

XX FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;  
KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.  
XX Homo sapiens.

OS Homo sapiens.

XX WO200118055-A1.

PN 15-MAR-2001.

XX 31-AUG-2000; 2000WO-US20807.

XX 10-SEP-1999; 99US-0153339.

XX (ELIL ) LILLY & CO ELI.

XX PI Atkinson PR, Tian Y, Witcher DR;

XX WPI; 2001-273382/28.

XX Compositions comprising a divalent metal cation and a FAS Ligand  
XX Inhibitory Protein (FLINT), for reducing or inducing aggregation of  
XX FLINT and for treating diseases involving FasL/Fas and/or  
XX LIGHT/LT-beta-R receptor interactions -

XX Example 1; Page 39-40; 44pp; English.

XX The present sequence represents a mature FLINT (FAS Ligand Inhibitory  
XX Protein) polypeptide. The specification describes a composition  
XX comprising a divalent metal cation and FLINT protein. The composition  
XX is used either for reducing, reversing or eliminating aggregation and  
XX precipitation of FLINT or for inducing oligomerisation or aggregation  
XX of FLINT molecules. They can be used for purifying FLINT and/or  
XX maintaining FLINT in solution. The compositions are used to treat  
XX and/or prevent disorders associated with the binding of Fas to FasL  
XX and/or LIGHT to the LTbetaR and/or TR2/HVEM receptors. Uses include the  
XX treatment of acute liver failure and cerebral ischemia and the prevention  
XX of apoptosis.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;  
Best Local Similarity 100.0%; Pred. No. 8.5e-115; Indels 0; Gaps 0;  
Matches 271; Conservative 0; Mismatches 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 60  
DB 1 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPPRHYTFQWNYLERCR 60  
QY 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120  
DB 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120  
QY 121 CQCPPGTFSASSSSSQCPHRNCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180  
DB 121 CQCPPGTFSASSSSSQCPHRNCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180  
QY 181 ECERAVIDFVAFQDISIKRLQRLLOALEAPEGWGTPPRAGRAALQLKLRRLTELLGAQD 240  
DB 181 ECERAVIDFVAFQDISIKRLQRLLOALEAPEGWGTPPRAGRAALQLKLRRLTELLGAQD 240

QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271  
 DB 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271

RESULT 8

AAB68047  
 ID AAB68047 standard; protein; 271 AA.

AC AAB68047;

DT 29-JUN-2001 (first entry)

DE Amino acid sequence of a human mature FLINT polypeptide.

XX FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;  
 XX Fas ligand; acute liver failure; cerebral ischemia; apoptosis.

OS Homo sapiens.

PN WO200118041-A2.

PD 15-MAR-2001.

PF 31-AUG-2000; 2000WO-US20805.

PR 10-SEP-1999; 99US-0153445.

PA (ELIL ) LILLY & CO ELI.

PI Atkinson PR, Tian Y, Witcher DR;

DR WPI; 2001-273381/28.

XX Compositions comprising a divalent metal cation and a FAS ligand  
 PT Inhibitory Protein (FLINT), for reducing or inducing aggregation of  
 PT FLINT and for treating diseases involving FasL/Fas and/or  
 PT LIGHT/Lt-beta-R receptor interactions -

PS Disclosure; Page 30-31; 33pp; English.

XX The present sequence represents a human mature FLINT (FAS ligand  
 CC Inhibitory Protein) polypeptide. The specification describes a  
 CC composition comprising a divalent metal cation and FLINT protein. The  
 CC composition is used either for reducing, reversing or eliminating  
 CC aggregation and precipitation of FLINT or for inducing oligomerisation  
 CC or aggregation of FLINT molecules. They can be used for purifying FLINT  
 CC and/or maintaining FLINT in solution. The compositions are used to treat  
 CC and/or prevent disorders associated with the binding of Fas to FasL  
 CC and/or LIGHT to the lTbetar and/or TR2/HVEM receptors. Uses include the  
 CC treatment of acute liver failure and cerebral ischemia and the prevention  
 CC of apoptosis.

SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;

Best Local Similarity 100.0%; Pred. No. 8.5e-115; Mismatches 0; Indels 0; Gaps 0;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTPYPMRDATGRLVCAQCPPTGVQPCRRDPTTCGCPRRHYTOFNNYLERCR 60

DB 1 VAEPTPYPMRDATGRLVCAQCPPTGVQPCRRDPTTCGCPRRHYTOFNNYLERCR 60

QY 61 YCNVLGGEREEERACHATNRAACRCRTGFFAHAGFCLHASCPPGAGVIAPGPSQNTQ 120

DB 61 YCNVLGGEREEERACHATNRAACRCRTGFFAHAGFCLHASCPPGAGVIAPGPSQNTQ 120

QY 121 CQCPPTGTSASSSSSEQCPHRCNTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGAE 180

DB 121 CQCPPTGTSASSSSSEQCPHRCNTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGAE 180

QY 181 ECERAVIDVAFODISIKRLQRLQLALEAPEGWPTRAGRALQLKLRRLTELLGAOD 240

DB 181 ECERAVIDVAFODISIKRLQRLQLALEAPEGWPTRAGRALQLKLRRLTELLGAOD 240  
 QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271  
 DB 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271

RESULT 9

AAB74465  
 ID AAB74465 standard; protein; 271 AA.

AC AAB74465;

DT 30-MAY-2001 (first entry)

DE Human FLINT mature protein.

XX Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;  
 XX inflammatory disease.

OS Homo sapiens.

PN WO200118202-A2.

PD 15-MAR-2001.

PF 31-AUG-2000; 2000WO-US20806.

PR 10-SEP-1999; 99US-0153433.

PA (ELIL ) LILLY & CO ELI.

PI Atkinson PR, Tian Y, Witcher DR;

DR WPI; 2001-257796/26.

XX Compositions useful for reducing/inducing aggregation of a FLINT analog  
 PT comprise a divalent metal cation and a protease-resistant FAS ligand  
 PT Inhibitory Protein (FLINT) analog -

PS Claim 4; Page 41-42; 44pp; English.

XX The present invention describes a composition comprising a divalent metal  
 CC cation associated with a protease resistant Fas ligand inhibitory protein  
 CC (FLINT) analogue. The composition is useful in the treatment of diseases  
 CC associated with Fas binding to its ligand, such as acute liver failure,  
 CC inflammatory diseases, cerebral ischemia and apoptosis. The present  
 CC sequence is the mature FLINT protein.

SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 22; Length 271;

Best Local Similarity 100.0%; Pred. No. 8.5e-115; Mismatches 0; Indels 0; Gaps 0;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTPYPMRDATGRLVCAQCPPTGVQPCRRDPTTCGCPRRHYTOFNNYLERCR 60

DB 1 VAEPTPYPMRDATGRLVCAQCPPTGVQPCRRDPTTCGCPRRHYTOFNNYLERCR 60

QY 61 YCNVLGGEREEERACHATNRAACRCRTGFFAHAGFCLHASCPPGAGVIAPGPSQNTQ 120

DB 61 YCNVLGGEREEERACHATNRAACRCRTGFFAHAGFCLHASCPPGAGVIAPGPSQNTQ 120

QY 121 CQCPPTGTSASSSSSEQCPHRCNTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGAE 180

DB 121 CQCPPTGTSASSSSSEQCPHRCNTALGLALNVPGSSSHDTLCTSGTFPLSTRVPGAE 180

QY 181 ECERAVIDVAFODISIKRLQRLQLALEAPEGWPTRAGRALQLKLRRLTELLGAOD 240

DB 181 ECERAVIDVAFODISIKRLQRLQLALEAPEGWPTRAGRALQLKLRRLTELLGAOD 240

QY	1	VAETPTVPRWDAETGERLCAVCAQPPGTFVORPCRRDSPTTCGCPRRHYTFWNYLERCR	60
Db	30	VAETPTVPRWDAETGERLCAVCAQPPGTFVORPCRRDSPTTCGCPRRHYTFWNYLERCR	89
QY	61	YCNVLGGERBEERAAACHATNNRACRTGTGFPAHAGFCLEHASPPGAGVLAAGTPSNTQ	120
Db	90	YCNVLGGERBEERAAACHATNNRACRTGTGFPAHAGFCLEHASPPGAGVLAAGTPSNTQ	149

Qy	1	VAEPTYPWRDAEUGERLVCAQCPG	1	CAFRKNS	60
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Qy	1	VAEPTYPWRDAEUGERLVCAQCPG	1	CAFRKNS	60
Db	1	VAEPTYPWRDAEUGERLVCAQCPG	1	CAFRKNS	60
Qy	61	YCNVLCGBREBARACHATHNRCRCPTG	61	FAHAGFCLEHASCPPGAGVIA	120
Db	61	YCNVLCGBREBARACHATHNRCRCPTG	61	FAHAGFCLEHASCPPGAGVIA	120
Qy	61	YCNVLCGBREBARACHATHNRCRCPTG	61	FAHAGFCLEHASCPPGAGVIA	120
Db	61	YCNVLCGBREBARACHATHNRCRCPTG	61	FAHAGFCLEHASCPPGAGVIA	120
Qy	121	CAQCPGPTAAGS	121	SSSGSCGCGHNTA	180
Db	121	CAQCPGPTAAGS	121	SSSGSCGCGHNTA	180

QY 121 CQPCPGTFSASSSSSQCPHNRCTALGLALNVGSSSHDTLCTSGTGFPLSTRVPGAE 180  
 Db 150 CQPCPGTFSASSSSSQCPHNRCTALGLALNVGSSSHDTLCTSGTGFPLSTRVPGAE 209  
 QY 181 ECEBAVIDFVAFODISIKRLQRLQALEAPEGWPPTPRAGRAALQKLRRLTELLGAQD 240  
 Db 210 ECEBAVIDFVAFODISIKRLQRLQALEAPEGWPPTPRAGRAALQKLRRLTELLGAQD 269  
 QY 241 GALLVRLQLQALRVARMGELRSYVERFLPVH 271  
 Db 270 GALLVRLQLQALRVARMGELRSYVERFLPVH 300  
 RESULT 12  
 AAM63622  
 ID AAM63622 standard; Protein; 300 AA.  
 AC AAM63622;  
 XX  
 DT 26-OCT-1998 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-6 alpha protein.  
 XX  
 KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;  
 KM endothelial cells; keratinocytes; normal prostate; apoptosis;  
 KM prostate tumour tissue.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..30  
 FT Protein 31..300  
 FT /note= "TNFR-6 alpha"  
 FT Region 31..282  
 FT /note= "Soluble extracellular domain"  
 XX  
 PN MO9830694-A2.  
 XX  
 PD 16-JUL-1998.  
 XX  
 PF 13-JAN-1998; 98MO-US00153.  
 XX  
 PR 14-JAN-1997; 97US-0035496.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;  
 XX WPI: 1998-399142/34.  
 DR N-PSDB; AAV39085.  
 XX  
 PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
 PT the diagnosis of immune system-related disorder(s)  
 XX  
 PS Claim 20; Fig 1; 91pp; English.  
 XX  
 CC The present sequence represents the human tumour necrosis factor  
 CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides  
 CC for the TNFR-6 beta protein (AAM63623). TNFR-6 alpha and TNFR-6 beta  
 CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
 CC are expressed in endothelial cells, keratinocytes, normal prostate and  
 CC prostate tumour tissue. For a number of disorders of these cells,  
 CC particularly of the immune system, substantially altered (whether  
 CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene  
 CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta  
 CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
 CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
 CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are  
 CC also claimed to be useful for identifying ligands which may be useful  
 CC in the treatment of apoptosis related disorders.  
 CC  
 XX Sequence 300 AA;  
 XX

Query Match 100.0%; Score 1491; DB 19; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VAEPTPMWDAETGERLVCACQCPGTFFVORPCRBDSPITCGPCPPRHYYQFMWYLERCR 60  
 Db 30 VAEPTPMWDAETGERLVCACQCPGTFFVORPCRBDSPITCGPCPPRHYYQFMWYLERCR 89  
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 Db 90 YCNVLCGEREEERACIATNNRACRCRTGFFAHAGFCLBHASCPPAGGVLAFTGPSQNTQ 149  
 QY 121 CQPCPGTFSASSSSSQCPHNRCTALGLALNVGSSSHDTLCTSGTGFPLSTRVPGAE 180  
 Db 150 CQPCPGTFSASSSSSQCPHNRCTALGLALNVGSSSHDTLCTSGTGFPLSTRVPGAE 209  
 QY 181 ECEBAVIDFVAFODISIKRLQRLQALEAPEGWPPTPRAGRAALQKLRRLTELLGAQD 240  
 Db 210 ECEBAVIDFVAFODISIKRLQRLQALEAPEGWPPTPRAGRAALQKLRRLTELLGAQD 269  
 QY 241 GALLVRLQLQALRVARMGELRSYVERFLPVH 271  
 Db 270 GALLVRLQLQALRVARMGELRSYVERFLPVH 300  
 RESULT 13  
 AAY03099  
 ID AAY03099 standard; Protein; 300 AA.  
 AC AAY03099;  
 XX  
 DT 09-DEC-1999 (first entry)  
 XX  
 DE Human lung TNF-receptor protein.  
 XX  
 KW Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;  
 KM detection; immunosassay; diagnosis; disease; immune system; tumour;  
 KM osteogenic system; cardiovascular system; central nervous system; asthma;  
 KM peripheral nervous system; transplant incompatibility; antitumor;  
 KM rheumatoid arthritis; antiasthmatic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 134..1036  
 FT /\*tag= a  
 FT /product= "TNF-receptor"  
 XX  
 PN DE19809978-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 09-MAR-1998; 98DE-1009978.  
 XX  
 PR 09-MAR-1998; 98DE-1009978.  
 XX  
 PA (BADT ) BASF AG.  
 XX  
 PI Kroeger B;  
 XX WPI: 1999-519473/44.  
 DR N-PSDB; AAZ09998.  
 XX  
 PT New soluble member of tumor necrosis factor receptor family, useful for  
 PT identification specific modulators and for treating disease e.g. tumors  
 XX  
 PS Claim 1; Page 8-9; 10pp; German.  
 XX  
 CC This invention describes a novel tumour necrosis factor (TNF) receptor  
 CC (I) isolated from human lung tissue. (I) is used; (i) to raise specific  
 CC antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands

CC (A), potential therapeutic agents; and (iii) therapeutically (optionally  
 CC expressed from a gene therapy vector) in conditions associated with a  
 CC deficit of (I). Ab are used: (a) for qualitative or quantitative  
 CC detection of (I) in standard immunoassays (for diagnosis of disease, or  
 CC susceptibility, or for monitoring); and (b) as therapeutic inhibitors in  
 CC cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is  
 CC used: (A) for recombinant production of (I); (B) also its oligonucleotide  
 CC fragments, in standard hybridization and/or amplification assays; (C) as  
 CC source of antisense molecules or ribozymes; and (D) to produce transgenic  
 CC animals (for studying (patho)physiology of (I)). Diseases possibly  
 CC associated with under- or over-expression of (I) are those of the immune,  
 CC osteogenic, cardiovascular and central or peripheral nervous systems,  
 CC tumors, transplant incompatibility, asthma and rheumatoid arthritis. The  
 CC products of the invention have antitumor, antiasthmatic and  
 CC antiarthritic activity. This sequence represents the TNF-receptor of the  
 CC invention.

XX SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPRRHYTFQWNYLERCR 60  
 DB 30 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPRRHYTFQWNYLERCR 89  
 QY 61 YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120  
 DB 90 YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 149  
 QY 121 CQPCPPGTFSSSSSQCPHRNCTALGLALNVPGSSSHDTLTCTSGTGPLSTRVPGAE 180  
 DB 150 CQPCPPGTFSSSSSQCPHRNCTALGLALNVPGSSSHDTLTCTSGTGPLSTRVPGAE 209  
 QY 181 ECERAVIDFVAFQDISIKRLQLQALEAPEGNGPTPRAGRAALQLKRRRLTELLGAQD 240  
 DB 210 ECERAVIDFVAFQDISIKRLQLQALEAPEGNGPTPRAGRAALQLKRRRLTELLGAQD 269

RESULT 14  
 AAY42182  
 ID AAY42182 standard; Protein; 300 AA.

XX AC AAY42182;

XX 17-DEC-1999 (first entry)

DE Human FLINT #1 protein sequence.

XX Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;  
 KW apoptosis; inflammation; cancer; diabetes; acute liver failure;  
 KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;  
 KW reperfusion-associated injury; aplastic anaemia; differentiation;  
 KW growth; myelodysplastic syndrome; pancytopenic condition;  
 KW myocardial ischaemia.

OS Homo sapiens.

XX WO9950413-A2.

XX 07-OCT-1999.

XX 30-MAR-1999; 99WO-US06797.

XX 30-MAR-1998; 98US-0079856.

XX 20-MAY-1998; 98US-0086074.

XX 09-SEP-1998; 98US-0099643.

XX 17-DEC-1998; 98US-0112577.

PR 18-DEC-1998; 98US-0112703.  
 PR 18-DEC-1998; 98US-0112933.  
 PR 22-DEC-1998; 98US-0113407.  
 XX (ELIL) LILLY & CO ELI.  
 XX Humol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;  
 PI Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;  
 PI Song HY, Wang J, Wu X, Zuckerman SH;  
 XX WPI; 1999-591319/50.  
 DR N-PSDB; AA225375.  
 XX Use of mature FLINT for treating acute liver failure, inflammation,  
 PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic  
 PT and proinflammatory activity  
 XX Claim 30; Fig 1; 99pp; English.

XX The present invention describes therapeutic applications of mature FLINT  
 CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT  
 CC (mFLINT), which is a member of the tumour necrosis factor receptor  
 CC superfamily, is used for treating acute liver failure, inflammation of  
 CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated  
 CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated  
 CC injury or disorder such as hypercoagulation (including use with  
 CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury  
 CC or disorder, Type I diabetes, cancer, cell damage or damage to an  
 CC innocent bystander tissue that is induced by a chemotherapeutic agent or  
 CC therapeutic irradiation, treating haematopoietic progenitor cells that  
 CC have been exposed to therapeutic radiation or chemotherapy, aplastic  
 CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is  
 CC also used for promoting the growth or differentiation of a haematopoietic  
 CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte  
 CC resulting from abnormal myocardial ischaemia. The present sequence  
 CC represents human FLINT.

XX SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 20; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-115;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGGTFVQPCRRDSPTTCGCPRRHYTFQWNYLERCR 60  
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 QY 61 YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120  
 DB 90 YCNVLCGEREEERACHATHNACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 149  
 QY 121 CQPCPPGTFSSSSSQCPHRNCTALGLALNVPGSSSHDTLTCTSGTGPLSTRVPGAE 180  
 DB 150 CQPCPPGTFSSSSSQCPHRNCTALGLALNVPGSSSHDTLTCTSGTGPLSTRVPGAE 209  
 QY 181 ECERAVIDFVAFQDISIKRLQLQALEAPEGNGPTPRAGRAALQLKRRRLTELLGAQD 240  
 DB 210 ECERAVIDFVAFQDISIKRLQLQALEAPEGNGPTPRAGRAALQLKRRRLTELLGAQD 269  
 QY 241 GALLVRLQLQALRVARMFGLERSVRERFLPVH 271  
 DB 270 GALLVRLQLQALRVARMFGLERSVRERFLPVH 300

RESULT 15

AAY17479

ID AAY17479 standard; Protein; 300 AA.

XX AC AAY17479;

XX 02-AUG-1999 (first entry)

XX Mammalian tumour necrosis factor receptor OPG-2.

XX Tumour necrosis factor receptor; TNF receptor; OPG-2; Paget's disease;  
KM osteopenic disorder; osteoclast activity; primary osteoporosis;  
KM hyperglycaemia; osteolytic metastasis; immune response; cancer.  
XX  
OS Mammalia.  
XX WO9226977-A1.  
PN  
XX  
PD 03-JUN-1999.  
XX  
PF 24-NOV-1998; 98WO-US25065.  
XX  
PR 17-FEB-1998; 98US-0074896.  
PR 24-NOV-1997; 97US-0066446.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
PI Tschopp J;  
XX  
DR WPI: 1999-347693/29.  
DR N-PSDB; AAX76052.  
XX  
PT New tumour necrosis factor family receptor OPG-2  
XX  
PS Claim 1; Page 18; 22pp; English.  
XX  
CC The present sequence represents a mammalian tumour necrosis factor  
CC receptor, designated OPG-2. OPG-2, is a member of the tumour necrosis  
CC factor receptor family, and can be used: (i) to raise specific  
CC antibodies (Ab), (ii) to treat osteopenic disorders associated with  
CC excessive osteoclast activity, e.g. primary osteoporosis, Paget's  
CC disease, hyperglycaemia of malignancy, or osteolytic metastases; (iii)  
CC for affinity purification of cognate ligands, and (iv) to screen for  
CC ligands (antagonists or agonists). Ab, or other OPG-2 blocking agents  
CC such as soluble forms of the protein, are used to prevent, or reduce  
CC severity of, an immune response, and for treating cancer. They can also  
CC be used in diagnostic assays. The nucleic acid sequence encoding OPG-2  
CC can be used as a probe to isolate related sequences from other species.  
XX  
SQ Sequence 300 AA;  
  
Query Match 100.0%; Score 1491; DB 20; Length 300;  
Best Local Similarity 100.0%; Pred. No. 9.6e-115;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VAETPTYPMDAETGERLVCAQCPTGTFVORPCRDSPTTCGCPPHRYTQFMNYLERCR 60  
DB 30 VAETPTYPMDAETGERLVCAQCPTGTFVORPCRDSPTTCGCPPHRYTQFMNYLERCR 89  
  
QY 61 YCNVLCGEREREERARACHTNRACRCRTGFFAHAGFCLHNASCPGAGVIAFGTSPONTQ 120  
DB 90 YCNVLCGEREREERARACHTNRACRCRTGFFAHAGFCLHNASCPGAGVIAFGTSPONTQ 149  
  
QY 121 CQPCPCTFASASSSSQCPHRCNTALGLALNVGSSSHDTLCTCTGFPPLSTRVPGAE 180  
DB 150 CQPCPCTFASASSSSQCPHRCNTALGLALNVGSSSHDTLCTCTGFPPLSTRVPGAE 209  
  
QY 181 EGERAVIDFAFODISIKRLQRLQALEAPGSGPTPRAGRAALQKLRRRLTELLGAOD 240  
DB 210 EGERAVIDFAFODISIKRLQRLQALEAPGSGPTPRAGRAALQKLRRRLTELLGAOD 269  
  
QY 241 GALLVRLLOALRVARMGRLERSVREPLPVH 271  
DB 270 GALLVRLLOALRVARMGRLERSVREPLPVH 300

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:16:55 ; Search time 21 Seconds  
(without alignments)  
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Perfect score: 1491  
Sequence: 1 VAEPTPYMRDAETGERLVC.....RVARMGLERSVREFLPVH 271

Scoring table: BLOSUM62  
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
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6: /cgn2\_6/prodata/2/1aa/Backfill1.pep:\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1491	100.0	300	2	US-08-794-796-2	Sequence 2, App1
2	1476.5	99.0	299	4	US-09-286-529-17	Sequence 17, App1
3	1034	69.3	211	4	US-09-286-529-20	Sequence 20, App1
4	841	56.4	153	4	US-09-286-529-2	Sequence 2, App1
5	440.5	29.5	401	3	US-08-974-022-6	Sequence 6, App1
6	440.5	29.5	401	4	US-09-042-785A-12	Sequence 12, App1
7	440.5	29.5	401	4	US-08-795-445A-6	Sequence 6, App1
8	440.5	29.5	401	4	US-08-974-186-6	Sequence 6, App1
9	440.5	29.5	401	4	US-08-795-446B-6	Sequence 6, App1
10	440.5	29.5	401	4	US-08-795-446B-6	Sequence 6, App1
11	440.5	29.5	401	4	US-09-153-927-1	Sequence 1, App1
12	440.5	29.5	401	4	US-09-072-993C-1	Sequence 1, App1
13	440.5	29.5	401	4	US-08-706-945D-18	Sequence 128, App1
14	425.5	28.5	401	3	US-08-974-022-2	Sequence 2, App1
15	425.5	28.5	401	4	US-08-795-445A-2	Sequence 2, App1
16	425.5	28.5	401	4	US-08-795-447A-2	Sequence 2, App1
17	425.5	28.5	401	4	US-08-974-186-2	Sequence 2, App1
18	425.5	28.5	401	4	US-08-795-446B-2	Sequence 2, App1
19	425.5	28.5	401	4	US-08-706-945D-124	Sequence 124, App1
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22	424.5	28.5	401	4	US-08-795-445A-4	Sequence 4, App1
23	424.5	28.5	401	4	US-08-795-447A-4	Sequence 4, App1
24	424.5	28.5	401	4	US-08-974-186-4	Sequence 4, App1
25	424.5	28.5	401	4	US-08-795-446B-4	Sequence 4, App1
26	424.5	28.5	401	4	US-08-706-945D-126	Sequence 126, App1
27	407	27.3	147	4	US-09-527-236A-20	Sequence 20, App1

28	394	26.4	174	4	US-08-706-945D-136	Sequence 136, App
29	385.5	25.9	364	4	US-08-706-945D-142	Sequence 142, App
30	374.5	25.1	364	4	US-08-706-945D-141	Sequence 141, App
31	373	25.0	139	4	US-08-706-945D-130	Sequence 130, App
32	342.5	23.0	461	4	US-09-042-785A-7	Sequence 7, App1
33	342.5	23.0	461	4	US-09-006-353A-4	Sequence 4, App1
34	342.5	23.0	461	1	US-09-573-986-4	Sequence 4, App1
35	340.5	22.8	461	4	US-08-385-229-2	Sequence 2, App1
36	340.5	22.8	461	2	US-08-650-000-2	Sequence 2, App1
37	340.5	22.8	461	4	US-08-477-347-3	Sequence 3, App1
38	340.5	22.8	461	4	US-08-476-862-2	Sequence 2, App1
39	340.5	22.8	461	6	5395760-2	Patent No. 5395760
40	335	22.5	227	3	US-08-974-022-48	Sequence 48, App1
41	335	22.5	227	4	US-08-795-445A-48	Sequence 48, App1
42	335	22.5	227	4	US-08-795-447A-48	Sequence 48, App1
43	335	22.5	227	4	US-08-974-186-48	Sequence 48, App1
44	335	22.5	227	4	US-08-795-446B-48	Sequence 48, App1
45	335	22.5	227	4	US-08-706-945D-134	Sequence 134, App

## ALIGNMENTS

RESULT 1  
US-08-794-796-2  
; Sequence 2, Application US/08794796  
; Patent No. 5885800  
; GENERAL INFORMATION:  
; APPLICANT: Emery, John  
; APPLICANT: Tan, KB  
; APPLICANT: Truneh, Alem  
; APPLICANT: Young, Peter  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794,796  
; FILING DATE: 04-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: GH50000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4026  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 300 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-794-796-2  
Query Match 100.0%; Score 1491; DB 2; Length 300;  
Best Local Similarity 100.0%; Pred. No. 3e-124;

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Db	30	VAETPTYWRDAETGERL	VCAQCPGTFVQRP	CCRRDSPTTCGCP	PPRHYTFQWNYL	RCR	89			
QY	61	YCNVLGGEREEERACHA	TNHRACRGTGFFAHAG	FCLEHASC	PPGAGVIAGTP	SQNTQ	120			
Db	90	YCNVLGGEREEERACHA	TNHRACRGTGFFAHAG	FCLEHASC	PPGAGVIAGTP	SQNTQ	149			
QY	121	CQCPPGTFFASSSSSQ	CQPHRNC	TALGLALN	VPGSSSHDTLCT	CTCGFP	PLSTRV	PGAE	180	
Db	150	CQCPPGTFFASSSSSQ	CQPHRNC	TALGLALN	VPGSSSHDTLCT	CTCGFP	PLSTRV	PGAE	209	
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QY	241	GALLVRLQLALRVARMP	GLERSV	REFLPVH	271					
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RESULT 2
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Triboulev
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-17

```

Query Match	99.0%;	Score	1476.5;	DB	4;	Length	299;
Best Local Similarity	99.6%;	Pred.	No. 5.7e-133;				
Matches	270;	Conservative	0;	Mismatches	13;	Indels	1;
Gaps	1;						
QY	1	VAETPTYPWDAETGERLVCACQCPGTFVQRPCCRRDSTTTCGCPPPHRYTQFWNYLRCR	60				
Db	30	VAETPTYPWDAETGERLVCACQCPGTFVQRPCCRRDSTTTCGCPPPHRYTQFWNYLRCR	89				
QY	61	YCNVLCGEREEBAAACHATHNRACRCRTGTFPAHAGFCLEHASCPPGAGVIAPGTPSQNTQ	120				
Db	90	YCNVLCGEREEBAAACHATHNRACRCRTGTFPAHAGFCLEHASCPPGAGVIAPGTPSQNTQ	149				
QY	121	CQPCPGCTFGASSSSSEQCPHRNCTALGLALNVPGSSSHDCTLCTCTGFPPLSTRVPGA	180				
Db	150	CQPCPGCTFGA-SSSSSEQCPHRNCTALGLALNVPGSSSHDCTLCTCTGFPPLSTRVPGA	208				
QY	181	ECERAVIDFVAFODISIKRLQRLLOALEAPGEGWPTPRAGRAALQLKURRLTELLGAQD	240				
Db	209	ECERAVIDFVAFODISIKRLQRLLOALEAPGEGWPTPRAGRAALQLKURRLTELLGAQD	268				
QY	241	GALLVRLLOALRVARMFGLERSVRFPLFVH	271				
Db	269	GALLVRLLOALRVARMFGLERSVRFPLFVH	299				

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RESULT 3
US-09-286-529-20
; Sequence 20, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES

```

```

; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 211
; TYPE: prt
; ORGANISM: Homo sapien
US-09-286-529-20

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Query Match	69.3%; Score 1034; DB 4; Length 211;
Best Local Similarity	98.9%; Pred. No. 4.8e-84;
Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 VAETPTPWDAETGERLVCQAQPFGTFVORPCRDRSPPTTCGCPPPHHYTFQWNYLERCR 60 
Dd	30 VAETPTPWDAETGERLVCQAQPFGTFVORPCRDRSPPTTCGCPPPHHYTFQWNYLERCR 89 
Qy	61 YCNVLCSEREEARACHATNACRCKTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120 
Dd	90 YCNVLCSEREEARACHATNACRCKTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149 
Qy	121 CQPCPGCTFSASSSSSQOPHRNCTALGHALNVPGSSSHDTLCSTCGPLSTRFVPQAE 180 
Dd	150 CQPCPGCTFSASSSSSQOPHRNCTALGHALNVPGSSSHDTLCSTCGPLSTRFVEGP 209 
Qy	181 E 181
Dd	210 E 210

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RESULT 4
US-09-286-529-2
; Sequence 2, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
; US-09-286-529-2

```

	Query Match	56.4%	Score 841;	DB 4;	Length 153;	
	Best Local Similarity	100.0%;	Pred. No. 3.7e-67;			
	Matches 153; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
<hr/>						
Qy	56 LERCYCNVLGEEEEERACHATHNPRACRCRTGFFAHAGFCLEHASCPPGAGVIAEGTP	115				
Dd	1 LERCYCNVLGEEEEERACHATHNPRACRCRTGFFAHAGFCLEHASCPPGAGVIAEGTP	60				
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Qy	116 SONTQCPCPPTGFSASSSSSECOCPHRNCTALGLANVPGSSSHDPLCTCSCTGFPLSTR	175				
Dd	61 SONTQCPCPPTGFSASSSSSECOCPHRNCTALGLANVPGSSSHDPLCTCSCTGFPLSTR	120				
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Qy	176 VPGBECERAVIDFVAFQDISIKRLQLLOALE	208				
Dd	121 VPGBECERAVIDFVAFQDISIKRLQLLOALE	153				

RESULT 5  
US-08-974-022-6  
; Sequence 6, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.

APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
City: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022-6

Query Match 29.5%; Score 440.5; DB 3; Length 401;  
Best Local Similarity 41.2%; Pred. No. 2.9e-31;  
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYWRDAETGERLVCAQCPGPTGVORPCRRDSPPTGCPGPPRHYYTFWVYLERCRYCNV 64  
DB 26 PKYHYDEBETSHOLGCKCPGTYLKQHTAKMKTVCAPCPDHYTDSMHTSDCLYCSP 85  
QY 65 LCGREBEARACHATNHRACRGTGFFAHAGFCLFHASCPRGAGVIAPGTPSONTQOPC 124  
DB 86 VCKELQYVKQECNTHNRVCEKGRYLEIEFCLKHRSCEPGFVGVAQGPERRVTCKRC 145  
QY 125 PPGTFSSASSSSBQCPHRTCTALGLALNVPSSSHDTLCTSCGFFLSTRVPGAEE--C 182  
DB 146 PDGFFSMETSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CGNSSESTQKCGIDVTLC 202  
QY 183 ERAVIDF 189  
DB 203 EEAFFRF 209

RESULT 6  
US-09-042-785A-12  
Sequence 12, Application US/09042785A  
Patent No. 6194151  
GENERAL INFORMATION:  
APPLICANT: Busfield, Samantha J  
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
City: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,785A  
FILING DATE: 17-MAR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/938,896  
FILING DATE: 26-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MEI-001CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-042-785A-12

Query Match 29.5%; Score 440.5; DB 4; Length 401;  
Best Local Similarity 41.2%; Pred. No. 2.9e-31;  
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYWRDAETGERLVCAQCPGPTGVORPCRRDSPPTGCPGPPRHYYTFWVYLERCRYCNV 64  
DB 26 PKYHYDEBETSHOLGCKCPGTYLKQHTAKMKTVCAPCPDHYTDSMHTSDCLYCSP 85  
QY 65 LCGREBEARACHATNHRACRGTGFFAHAGFCLFHASCPRGAGVIAPGTPSONTQOPC 124  
DB 86 VCKELQYVKQECNTHNRVCEKGRYLEIEFCLKHRSCEPGFVGVAQGPERRVTCKRC 145  
QY 125 PPGTFSSASSSSBQCPHRTCTALGLALNVPSSSHDTLCTSCGFFLSTRVPGAEE--C 182  
DB 146 PDGFFSMETSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CGNSSESTQKCGIDVTLC 202  
QY 183 ERAVIDF 189  
DB 203 EEAFFRF 209

RESULT 7  
US-08-795-445A-6  
Sequence 6, Application US/08795445A  
Patent No. 6284485  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
City: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,445A  
FILING DATE:



Db 86 VCKELQVYKQECNTHNRVCECKEGRYLEIFCLKHSRCPGFGVQAGTBERNTVCRC 145  
QY 125 PPGTSSASSSSSECOCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVGAEE--C 182  
Db 146 PDGFFSNSTSSKAPCRKHTNCSVFGLLTLQKGNATHDNI---CGSNGSESTQKCGIDVTLC 202  
QY 183 ERAVIDF 189  
Db 203 EEAFFRF 209

RESULT 10  
US-08-795-446B-6  
; Sequence 6, Application US/08795446B  
; Patent No. 6288032  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,446B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 401 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-795-446B-6

Query Match 29.5%; Score 440.5; DB 4; Length 401;  
Best Local Similarity 41.2%; Pred. No. 2.9e-31;  
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYPMRDAETGERLIVCAQCPGTFVQRCRRDSPTTCGCPFRHYTOFMWYLERGRYCNV 64  
Db 26 PKYLHYDEFTSHQLCDKCPGTYLKQHTAKWTVCAPCPDHYTDSMTSDCLYCSP 85  
QY 65 LCGREEREARACHATHNRACRGTGFPAHAGFCLEHASCSPGAGVIAPGTBSQNTQOCP 124  
Db 86 VCKELQVYKQECNTHNRVCECKEGRYLEIFCLKHSRCPGFGVQAGTBERNTVCRC 145  
QY 125 PPGTSSASSSSSECOCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVGAEE--C 182  
Db 146 PDGFFSNSTSSKAPCRKHTNCSVFGLLTLQKGNATHDNI---CGSNGSESTQKCGIDVTLC 202  
QY 183 ERAVIDF 189  
Db 203 EEAFFRF 209

RESULT 11  
US-09-153-927-1  
; Sequence 1, Application US/09153927A  
; Patent No. 6297022  
; GENERAL INFORMATION:  
; APPLICANT: McDonnell, Peter C.  
; APPLICANT: Young, Peter R.  
; APPLICANT: Zou, Jun  
; TITLE OF INVENTION: A method of identifying agonists and  
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3  
; FILE REFERENCE: GH50031  
; CURRENT APPLICATION NUMBER: US/09/153,927A  
; CURRENT FILING DATE: 1998-09-16  
; EARLIER APPLICATION NUMBER: 60/061,334  
; EARLIER FILING DATE: 1997-10-08  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: Human  
; US-09-153-927-1

Query Match 29.5%; Score 440.5; DB 4; Length 401;  
Best Local Similarity 41.2%; Pred. No. 2.9e-31;  
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYPMRDAETGERLIVCAQCPGTFVQRCRRDSPTTCGCPFRHYTOFMWYLERGRYCNV 64  
Db 26 PKYLHYDEFTSHQLCDKCPGTYLKQHTAKWTVCAPCPDHYTDSMTSDCLYCSP 85  
QY 65 LCGREEREARACHATHNRACRGTGFPAHAGFCLEHASCSPGAGVIAPGTBSQNTQOCP 124  
Db 86 VCKELQVYKQECNTHNRVCECKEGRYLEIFCLKHSRCPGFGVQAGTBERNTVCRC 145  
QY 125 PPGTSSASSSSSECOCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVGAEE--C 182  
Db 146 PDGFFSNSTSSKAPCRKHTNCSVFGLLTLQKGNATHDNI---CGSNGSESTQKCGIDVTLC 202  
QY 183 ERAVIDF 189  
Db 203 EEAFFRF 209

RESULT 12  
US-09-072-993C-1  
; Sequence 1, Application US/09072993C  
; Patent No. 6346388  
; GENERAL INFORMATION:  
; APPLICANT: Michael R. Bringham-Burke  
; APPLICANT: Peter R. Young  
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND  
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2  
; FILE REFERENCE: GH-50030  
; CURRENT APPLICATION NUMBER: US/09/072,993C  
; CURRENT FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/055,513  
; PRIOR FILING DATE: 1997-08-13  
; PRIOR APPLICATION NUMBER: 60/056,980  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/057,550  
; PRIOR FILING DATE: 1997-08-29  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 401  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
; US-09-072-993C-1

Query Match 29.5%; Score 440.5; DB 4; Length 401;  
Best Local Similarity 41.2%; Pred. No. 2.9e-31;



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,445A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-445A-2

Query Match 28.5%; Score 425.5; DB 4; Length 401;

Best Local Similarity 39.5%; Pred. No. 6, 2e-30;  
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;

QY 5 PTYPWRDAETGERLVCAQCPGGTFVQRPCRRDSPTTCGCPGCPRHHTQFMNYLERCRYCNV 64  
DB 26 PKYLHYDPETGRQLCDKCAPGYLKHQCTVRRKTLCVPCPDYSYTSWHTSDCYVCSP 85  
QY 65 LCGEREEREAACHTHNRACRCRTGFFAHAGFCLEHASCPGAGVIAPTPSQNTQCQPC 124  
DB 86 VKRELQTVKQECNRTHNRVCECEGRYLELEFCLKHRSCEPGLGVLAQGTPERNTVCCKRC 145  
QY 125 PCGTFSSASSSSSECCPHRNCTALGLALNVGSSSHDTLCTSGTGFPLSTRVPGAE--C 182  
DB 146 PDGFFSGETSSKAPCRKHTNCSSLGILLIQGNATHDNV---CSGNREATQNGSIDVTLC 202  
QY 183 ERAVIDFVAFODISIKRLRLQAL 207  
DB 203 EBAFFRFVAVPTKIIPNWLVLVDSL 227

Search completed: January 6, 2003, 11:21:35  
Job time : 22 secs

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XX Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micancovic R;  
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Wlitcher DR;  
PI Wroblewski WJ;  
XX WPI, 2000-656167/63.  
DR P-PSDB; AAB19334.  
XX FAS ligand inhibitory Protein analogs useful for treating abnormal  
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,  
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's  
PT disease  
XX  
XX  
PS Claim 37, Page 113, 114pp; English.  
XX  
XX The present sequence encodes a mature human FAS ligand inhibitory  
CC Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor  
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature  
CC FLINT protein is modified to produce analogues, which have greater  
CC potency, longer in vivo half-lives, decreased aggregation, decreased  
CC absorption onto surfaces, increased solubility and improved ease of  
CC formulation. The FLINT analogue is useful for treating a patient  
CC suffering from disease or condition relating to abnormal apoptosis such  
CC as acute lung injury, acute respiratory distress syndrome, pulmonary  
CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or  
CC Crohn's disease.  
XX  
XX  
SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 3,46e-77 Length: 813  
Score: 1491.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0  
  
US-09-936-024-1 (1-271) x AAA75999 (1-813)  
  
QY 1 ValAlaGluThrProThyThyProThyPArgAspAlaGluThrGlyGluArgLeuValCys 20  
Db 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCAGACAGAGGGAGCGGCTGGTGGC 60  
QY 21 AlaGlnCysProProGlyThyPheValGlnArgProCysArgArgSerProThrThr 40  
Db 61 GCCCAGTCCCCCGACGACCTTTGTGACGGCGCTGCCCGCAGACGCCACGACG 120  
QY 41 CysGlyProCysProProArgHisThyThyGlnPheTyrPheTyrLeuGluArgCysArg 60  
Db 121 TGTGGCCCGTGTCCACGCGGCACACTACAGCAGTTCTGGAACCTAGAGGGTGGCGC 180  
QY 61 TyrCysAsnValLeuGlyGlyGluArgGluGluGluAlaAlaGlyHisAlaThrHis 80  
Db 181 TACTGCAACGCTCTGTGGGAGAGGTAGAGAGGAGCGGCTTGGCAGCCAC 240  
QY 81 AsnArgAlaCysArgCysArgThyGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
Db 241 AACCTGCTGCTCCGCTGCGCAGCGGCTTCTTCCGCGACGCTGTTTCTTGGAGCAC 300  
QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThyProSerGlnAsnThrGln 120  
Db 301 GCATCGTGTCCACCTGGGCGCGGTGATGCCCCGGGACACCCAGCAGAACGCGAG 360  
QY 121 CysGlnProCysProProGlyThyThyPheSerAlaSerSerSerSerGlnGlnCysGln 140  
Db 361 TGCAGCGCTGCCCCCGAGGACCTTCTCAGCCAGCAGCTCAGAGTCCAGAGCGCAG 420  
QY 141 ProHisArgAsnCysThyAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160  
Db 421 CCCCACCGCACTGACGCGCTGGGCTTGGCCCTCAATGTCAGGCTTCTTCCCAT 480  
QY 161 AspThrLeuGlyThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
|||||

Db 481 GACACCTGTGCACACAGCTGCATGGCTTCCCTCAGCAGACAGAGTACAGAGCTGAG 540  
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleGlyArgLeu 200  
Db 541 GAGTGTAGCTGCTCCGCTGATGACTTTGTGCTTTCCAGACATCTCCATCAAGAGGCTG 600  
QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220  
Db 601 CAGCGGCTGCTGCAGGCGCTCGAGGCCCGGAGGGCTGGGCTCCGACACCAAGGGCGGCG 660  
QY 221 ArgAlaAlaLeuGlnLeuGlyLeuArgArgArgLeuThyGluLeuGlyAlaGlnAsp 240  
Db 661 CGCGCGGCTTGCAGCTGAACTGCTGCGGCTCAAGAGCTCTGGGGGCGCAGGAC 720  
QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260  
Db 721 GGGGCGCTGCTGCTGCGGCTGCTGAGGCGCTGGCGCTGGCAGAGTCCCGGCTGAG 780  
QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
Db 781 CGAGCGCTCGTAGCGGCTTCTCCTGTCAC 813  
  
RESULT 3  
AAA8730  
ID AAA8730 standard; cDNA; 813 BP.  
XX  
AC AAA8730;  
XX  
DT 05-FEB-2001 (first entry)  
XX  
XX Human FAS ligand inhibitor protein FLINT cDNA.  
DE  
XX FLINT, FAS ligand inhibitory protein; human; protease resistant;  
KW acute lung injury; acute respiratory distress syndrome;  
KW chronic obstructive pulmonary disease; pulmonary fibrosis;  
KW ulcerative colitis; therapy; organ transplantation; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN W0200058466-A2.  
XX  
PD 05-OCT-2000.  
XX  
PE 20-MAR-2000; 2000MO-US06418.  
XX  
XX 30-MAR-1999; 99US-0126839.  
PR 21-JUN-1999; 99US-0140073.  
PR 04-AUG-1999; 99US-0147071.  
PR 20-OCT-1999; 99US-0160524.  
PR 21-OCT-1999; 99US-0160669.  
PR 20-DEC-1999; 99US-0172744.  
PR 26-JAN-2000; 2000US-0178184.  
XX  
PA (BLIL ) Lilly & CO ELI.  
XX  
PI Micancovic R, Rathmachalam R, Wlitcher DR;  
XX WPI, 2000-664925/64.  
DR P-PSDB; AAB19705.  
XX  
XX Novel protease resistant FAS ligand inhibitory protein analogues  
PT resistant to in vivo or in vitro proteolysis at amino acid position 218  
PT of the mature protein, useful for treating autoimmune diseases  
XX  
XX Disclosure; Page 95; 100pp; English.  
XX  
XX The present sequence is that of cDNA coding for human FAS ligand  
CC inhibitory protein FLINT mature protein (see AAB19705). FLINT is a  
CC tumour necrosis factor receptor homologue that binds FAS ligand,  
CC preventing its interaction with FAS. This interaction is implicated  
CC in runaway apoptosis and inflammatory disease. FLINT also binds to  
CC LIGHT, a membrane-bound ligand, which may play a role in immune  
CC modulation and apoptosis. The invention relates to novel FLINT

CC analogues (see also AAB19706-09) that are resistant to proteolysis  
 CC by trypsin-like proteases between positions 218 and 219 of the  
 CC FLINT mature protein sequence. Nucleic acids, vectors and  
 CC transformed host cells for recombinant production of the analogues  
 CC are claimed. FLINT cDNA is used as a template for introducing the  
 CC required point mutations e.g. via PCR mutagenesis. The protease  
 CC resistant FLINT analogues are used to prevent or treat acute lung  
 CC injury, acute respiratory stress syndrome, ulcerative colitis,  
 CC chronic obstructive pulmonary disease, pulmonary fibrosis, to  
 CC inhibit T lymphocyte activation, and to facilitate organ  
 CC preservation for transplantation (claimed).  
 XX  
 SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:  
 Pred. No.: 3,46e-77 Length: 813  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-936-024-1 (1-271) x AAA88730 (1-813)

QY 1 ValAlaGluThrProThrTyrProThrArgAspAlaGluThrGlyGluArgLeuValCys 20  
 DB 1 GTGGCAAGAACACCCACCTACCCCTGGCGGGACGCAGACAGCGGGCGGTGGTGC 60  
 QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40  
 DB 61 GCCAGTGTCCCCCAGCGACCTTTGTGCAGCGCGCGTGGCGCGAGACAGCCCCAGCG 120  
 QY 41 CysGlyProCysProProArgHisTyrThrGlnPheThrAsnTyrLeuGluArgCysArg 60  
 DB 121 TGTGGCCCGTGTCCACCGGCCACTACACGAGTTCTGGAACCTACCTGGAGCGCTGCCGC 180  
 QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaAlaArgAlaCysHisAlaThrHis 80  
 DB 181 TACTGCAACGTCCTCTGCGGGGAGCGTGGAGGAGGCGCGCTTGCACGCCACCCAC 240  
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
 DB 241 AACCGTGCTTGGCGTCCGCGCACCGCGCTTCTTCGCGCACGCTGTTCTTGTGGAGCAC 300  
 QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120  
 DB 301 GCATCGTGTCCACCTGGTGGCGCGTGAITGCCCCGGGACCCCGGACGAGCAACACGCGAG 360  
 QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140  
 DB 361 TGCCAGCCCGTCCCCCAGCGACCTTCTCAGCCAGCAGCTCCAGCTCAGCAGGTGCCAG 420  
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160  
 DB 421 CCCCACCGCAACTGCACGCGCCCTGGGCCCTTGGCCCTCAATGTGCCAGGCTCTTCTCCCAT 480  
 QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
 DB 481 GACACCTGTGCACCAAGTGCATGGCTTCCCCCTCAGCACCAAGGTTACAGGAGCTGAG 540  
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200  
 DB 541 GAGTGTGAGCGTCCGCTCATCGACTTGTGGCTTCCAGGACATCTCCATCAAGAGGCTG 600  
 QY 201 GlnArgLeuGlnAlaLeuGluAlaProGluGlyTyrProThrProArgAlaGly 220  
 DB 601 CAGCGCTGTCTGACAGCCCTTCGAGGCCCGGAGGGCTGGGGTCCGACACACAGGCGGCG 660  
 QY 221 ArgAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240  
 DB 661 CGCGCGGCTTGCAGCTGAAGCTGCGTGGCGGCTCACGAGCTCTCTGGGGGCGCAGGAC 720  
 QY 241 GlyAlaLeuLeuValArgLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260

Db 721 GGGGGCGCTGCTGCTGCGGCTGCTGCGAGCGCTGCGGTGCCAGGATGCCCGGGCTGGAG 780  
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
 Db 781 CGGAGCGTCCGTGAGCGGCTTCTCCCTGTGCAC 813  
 RESULT 4  
 AAA51077  
 ID AAA51077 standard; DNA; 813 BP.  
 XX  
 AC AAA51077;  
 XX  
 DT 26-SEP-2000 (first entry)  
 XX  
 DE Mature human FLINT coding sequence.  
 KW FLINT; osteoprotegrin 3; OPG3; tumour necrosis factor receptor; TNFR;  
 KW FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;  
 KW anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;  
 KW anti-inflammatory; antibacterial; immunosuppressive; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT mat\_peptide 1..813  
 FT /\*tag= a  
 XX  
 PN WO200037094-A2.  
 PD 29-JUN-2000.  
 XX  
 PF 21-DEC-1999; 99WO-US30734.  
 XX  
 PR 22-DEC-1998; 98US-0113407.  
 PR 30-MAR-1999; 99WO-US06797.  
 PR 20-OCT-1999; 99US-0172239.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Cohen PJ, Posada JA, Wierda D;  
 XX  
 DR WPI, 2000-475441/41.  
 DR P-PSDB; AAY96598.  
 XX  
 PT Use of mature FLINT for treating e.g. acute respiratory distress  
 PT syndrome, ulcerative colitis or ischemic injury during organ  
 PT transplantation  
 XX  
 PS Example 8; Fig 3A-B; 125pp; English.  
 XX  
 CC Human FLINT (also known as osteoprotegrin 3) is a new tumour necrosis  
 CC factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and  
 CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas  
 CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for  
 CC treating acute respiratory distress syndrome, treating or inhibiting  
 CC ulcerative colitis, inhibiting ischemic injury during organ  
 CC transplantation or for organ preservation during transplantation. mFLINT  
 CC can also be used to treat acute liver failure, inflammation of the liver,  
 CC abnormal (hepatocyte) apoptosis, sepsis disorders associated with  
 CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,  
 CC damage to a cardiac myocyte resulting from abnormal myocardial ischemia,  
 CC Type I diabetes, cancer, damage to an innocent bystander tissue induced  
 CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,  
 CC myelodysplastic syndromes and pancytopenic conditions.  
 XX  
 SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Alignment Scores:  
 Pred. No.: 3,46e-77 Length: 813  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0  
 US-09-936-024-1 (1-271) x AA51077 (1-813)

QY 1 ValAlaGluThrProThrTyrProTTPArgAspAlaGluThrGlyGluArgLeuValCys 20  
 DB 1 GTGGCAAAACACCACCCTTACCCTTGGCGGAGACAGACAGGAGGAGCGGCTGGTGGC 60  
 QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40  
 DB 61 GCCCAGTGTCCCGCAGGACCTTTGTGACGCGCTGCCCGCAGACAGCCCAACGACG 120  
 QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTTPanTyrLeuGluArgCysArg 60  
 DB 121 TGTGGCCCGTGTCCACCGCGGCACTACACGAGTTCTGGAACTACCTGGACGCTGCCGC 180  
 QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgGalaCysHisAlaThrHis 80  
 DB 181 TACTGCAACGCTCTCTGGGAGCGTGAAGAGGACGAGCGGCTTGCACGCAACCCAC 240  
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
 DB 241 AACGTCCTGCGCTGCGCAGCGGCTTCTTCGCGACGCTGCTTCTGCTGGAGAC 300  
 QY 101 AlaserCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120  
 DB 301 GCATCGTGTCCACTGTGTGCGGCTGATTCCTCCGGGACCCCGACAGAAACAGCAG 360  
 QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140  
 DB 361 TGCACGCGTGTCCCGCAGGACCTTCTCACGACAGCTCCAGCTCAGACAGTGCAG 420  
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160  
 DB 421 CCCACCGCACTGACGCGCTGCGCTGCGCTCAATGCGCAGGCTTCTCCCTCCAT 480  
 QY 161 AsnThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyValAlaGlu 180  
 DB 481 GACACCTGTGACACAGCTGACTGGCTTCCCTCAGACACAGGATCCAGAGACTGAG 540  
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200  
 DB 541 GAGGTGAGCGCTGCGCTGATCGACTTGTGGCTTCCAGGACATCTCATCAAGAGCTG 600  
 QY 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGluGlyTTPGlyProThrProArgAlaGly 220  
 DB 601 CAGCGCTGTGACGAGCGCTTGAAGCCCGGAGGCTGGGGTCCGACACCAAGGCGGGC 660  
 QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuGluValAlaGlnAsp 240  
 DB 661 CGCGCGGCTTGCAGCTGAGCTGAGCTGCGGCGCTCAGCGAGCTCTGGGAGCGCAGAC 720  
 QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260  
 DB 721 GGGGCGTGTGCGGCTGCTGCAAGCGCTGCGCGCTGCGCGAGATCCCGGGCTGAG 780  
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
 DB 781 CGAGCGCTCGGTGAGCGCTTCTCCCTGTCAC 813

RESULT 5  
 AAD07380  
 ID AAD07380 standard; cDNA; 813 BP.  
 AC AAD07380;  
 XX 04-AUG-2001 (first entry)  
 XX  
 XX Human mature fas ligand inhibitory protein (FLINT) cDNA.  
 DE Human, fas ligand inhibitory protein; FLINT; acute lung injury; ALI;  
 XX Human, fas ligand inhibitory protein; FLINT; acute lung injury; ALI;  
 KW Human, fas ligand inhibitory protein; FLINT; acute lung injury; ALI;  
 KW TNFR; tumour necrosis factor receptor protein; ulcerative colitis; AIDS;

KW acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;  
 KW chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;  
 KW rheumatoid arthritis; fibropoliferative lung disease; ischaemia; sepsis;  
 KW fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;  
 KW chronic renal failure; graft-vs-host disease; cutaneous inflammation;  
 KW vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;  
 KW insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;  
 KW Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;  
 KW Down's syndrome; multiple sclerosis; cytostatic; nocrotropic;  
 KW neuroprotective; vasotrophic; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..813  
 FT /tag= a  
 FT /product= "Human mature fas ligand inhibitory protein  
 FT (FLINT)"  
 FT /note= "CDS does not include start and stop codon"  
 FT /partial  
 XX  
 XX MO200142463-AL.  
 XX  
 PD 14-JUN-2001.  
 PD  
 PF 29-NOV-2000; 2000MO-US30166.  
 XX  
 XX 07-DEC-1999; 99US-0169367.  
 PR 07-DEC-1999; 99US-0169381.  
 PR 07-DEC-1999; 99US-0169412.  
 PR 23-MAR-2000; 2000US-0191430.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 XX Lu J, Wilcher DR;  
 PI  
 XX WPI: 2001-381684/40.  
 DR P-PSDB; AAE03567.  
 XX  
 PT New FLINT polypeptide for treating and/or preventing acute lung injury,  
 PT acute respiratory distress syndrome, ulcerative colitis, and  
 PT graft-versus-host disease, comprises O-linked or N-linked  
 PT oligosaccharides -  
 XX  
 XX Example 1; Page 53; 60pp; English.  
 PS  
 XX The present sequence is human mature fas ligand inhibitory protein  
 CC (FLINT) cDNA. FLINT, a homologue of tumour necrosis factor receptor  
 CC protein (TNFR), binds fas ligand (FasL) and thereby preventing the  
 CC interaction of FasL with Fas. FLINT comprising O-linked or N-linked  
 CC oligosaccharides is useful for preventing or treating acute lung injury  
 CC (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,  
 CC chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),  
 CC to facilitate organ preservation for transplantation and to inhibit T  
 CC lymphocyte activation. FLINT is useful for treating and/or preventing  
 CC diseases such as rheumatoid arthritis, fibropoliferative lung disease,  
 CC fibrotic lung disease, acute lung injury, human immunodeficiency virus  
 CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-  
 CC host disease, cutaneous inflammation, vascular leak syndrome,  
 CC Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent  
 CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,  
 CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as  
 CC psoriasis, Down's syndrome, and multiple sclerosis.  
 XX  
 XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;  
 SQ

Alignment Scores:  
 Pred. No.: 3,46e-77 Length: 813  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-09-936-024-1 (1-271) x AAD07380 (1-813)

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QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 1 GTGGGAGAAACACCCACCTACCCCTGGCGGACGACAGACAGGGGAGCGGTGGTGTGC 60
QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 61 GCCCAGTCCCCCAGGCACCTTTGTGAGCGCGCTGCGCGAGACAGCCACGACG 120
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
Db 121 TGTGGCCCGTGTCCACCGGCCACTACAGCAGTTCGTGAACCTACCTGGAGCGCTGCCGC 180
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 181 TACTGCAAGTCTCTGCGGGAGCGTGTGAGGAGGACGCGGCTTGCCACGCCACCCAC 240
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 241 AACCGTGTGCGCGCTGCCGACCGGCTTCTTCGCGCACGCTGTTCTGCTTGGAGCAC 300
QY 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 301 GCATCGTGTCCACCTGTGCGCGCGTGTATGCCCCCGGCGACCCCCAGCAGACACGCGAG 360
QY 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
Db 361 TGGCAGCGTGGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGACGAGTGCAG 420
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
Db 421 CCCCACCGCAACTGCACGGCCCTGGCCCTGGCCCTCAATGTGCCAGGCTCTTCTCCCAT 480
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
Db 481 GACACCTGTGCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleValArgLeu 200
Db 541 GAGTGTGAGCGTCCGCTATCGACTTTGTGGCTTTCAGGACATCTCCATCAGAGGCTG 600
QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220
Db 601 CAGCGCTGTCTGCAGGCCCTCGAGGCCCGCGGCGCTGGGGTCCGACACCAAGGGCGGC 660
QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
Db 661 CGCGCGCGCTTGCAGCTGAAGCTGCTGCGCGCTCAGCGAGCTCCTGGGGCGCGAGGAC 720
QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
Db 721 GGGCGCGCTGTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 781 CGGAGCTCGTGTGAGCGCTTCTCCCTCGTGTGCAC 813
```

## RESULT 6

AAD27868

ID AAD27868 standard; DNA; 813 BP.

XX

AC AAD27868;

XX

DT 01-JUL-2002 (first entry)

XX

DE Human mature FLINT DNA.

XX

KW FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;

KW organ failure; liver; kidney; pancreas; inflammatory disease;

KW neutrophil; sepsis; acute respiratory distress syndrome;

KW acute lung injury; systemic inflammatory response syndrome; SIRS;

KW multiple organ dysfunction; MODS; human; gene; ds.

XX Homo sapiens.

OS

PH Key

FT CDS

FT Location/Qualifiers

FT 1..813

FT /\*tag= a

FT /product= "Mature FLINT protein"

FT /note= "Does not include start and stop codons"

FT /partial

XX

PN WO200209668-A2.

XX

PD 07-FEB-2002.

XX

PF 20-JUL-2001; 2001WO-211105.

XX

PR 02-AUG-2000; 2000US-222476P.

XX

PA (ELIL ) LILLY &amp; CO ELI.

XX

PI Micanovic R, Witcher DR;

XX

DR WPI; 2002-206149/26.

DR P-PSDB; AAE14578.

XX

PT Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,

PT useful for treating e.g. sepsis or respiratory distress syndrome,

PT involves pulmonary administration of a therapeutic amount of the FLINT

PT or FLINT analog -

XX

PS Disclosure; Page 30; 35pp; English.

XX

CC The invention relates to a new method of administering FLINT

CC (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary

CC administration of a therapeutic amount of the FLINT or FLINT analog.

CC The method enables systemic absorption of FLINT through lungs and

CC significantly reduces or eliminates the need for administering FLINT by

CC injection or other routes of administration. The method is useful in

CC treating disorders related to enhanced apoptosis (e.g. organ failure

CC in liver, kidneys and pancreas) and inflammatory diseases associated with

CC neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,

CC acute lung injury, systemic inflammatory response syndrome (SIRS) and

CC multiple organ dysfunction (MODS)). The method minimises the pain

CC and discomfort of injection methods. The present sequence is human

CC mature FLINT DNA.

XX

SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

XX

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-936-024-1 (1-271) x AAD27868 (1-813)

QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20

Db 1 GTGGGAGAAACACCCACCTACCCCTGGCGGACGACAGACAGGGGAGCGGTGGTGTGC 60

QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40

Db 61 GCCCAGTCCCCCAGGCACCTTTGTGAGCGCGCTGCGCGAGACAGCCACGACG 120

QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60

Db 121 TGTGGCCCGTGTCCACCGGCCACTACAGCAGTTCGTGAACCTACCTGGAGCGCTGCCGC 180

QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80



Db 448 TGCCACCGCTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGCAGAGTCCCGAG 507  
 Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160  
 Db 508 CCCACCGCAACTGCACGGCCCTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 567  
 Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
 Db 568 GACACCTGTGCACCACTGCAGCTTCCCTCCCTCAGCACCAGGTTACCGAGGTGAG 627  
 Qy 181 GluCyGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLeuArgLeu 200  
 Db 628 GAGTGTGAGGCTCCGCTCATGCTTGGCTTTCAGGACATCTCCATCAGAGGCTG 587  
 Qy 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrProThrProArgAlaGly 220  
 Db 688 CAGCGCTGTGCAGGCCCTCGAGGCCCGGAGGCTGGGGTCCGACCAAGGGCGGC 747  
 Qy 221 ArgAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240  
 Db 748 CGCGCGCTTGCAGCTGAAGCTGCGTGGCGGCTCAGCAGCTCCTGGGGCGCAGGAC 807  
 Qy 241 GlyAlaLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260  
 Db 808 GGGGCGCTGCTGTGGCTGCTGCGAGGCGCTGGCGTGGCCAGGATGCCCGGCTGGAG 867  
 Qy 261 ArgSerValArgGluArgPheLeuProValHis 271  
 Db 868 CGGAGGCTCGTGAGGCTTCTCTCCCTGTGCAC 900  
 RESULT 8  
 AAA53208  
 ID AAA53208 standard; cDNA; 900 BP.  
 XX  
 AC AAA53208;  
 XX  
 DT 03-JAN-2001 (first entry)  
 XX  
 DE Human Fas ligand inhibitor FLINT coding sequence.  
 XX  
 KW Human; Fas ligand inhibitor; FLINT; apoptosis; autoimmune disease;  
 KW inflammation; infectious disease; ischaemia; Alzheimer's disease;  
 KW Parkinson's disease; Crohn's disease; transplantation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..900  
 FT /\*tag= a  
 FT /product= "FLINT"  
 FT /partial  
 FT sig\_peptide 1..90  
 FT /\*tag= b  
 FT mat\_peptide 91..900  
 FT /\*tag= c  
 XX  
 PN WO200034782-A1.  
 XX  
 PD 15-JUN-2000.  
 XX  
 PF 07-DEC-1999; 99WO-US28696.  
 XX  
 PR 09-DEC-1998; 98US-0111575.  
 PR 09-DEC-1998; 98US-0111580.  
 PR 07-JAN-1999; 99US-0115069.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Rosteck PRJ, Song HY, Su EW;  
 XX  
 DR WPI: 2000-431379/37.  
 DR P-PSDB; AAB03621.  
 XX

PT Novel monkey Fas ligand inhibitor polypeptides, useful for treating  
 PT inflammatory or autoimmune disease such as rheumatoid arthritis,  
 PT infectious diseases such as chronic hepatitis, and  
 XX Ischaemia/Re-perfusion conditions -  
 PS Example 1; Page 88-91; 101pp; English.  
 XX  
 CC The present sequence is the coding sequence of the human Fas ligand  
 CC inhibitor (FLINT). The FLINT protein is involved in cell-specific  
 CC apoptosis, and can be used to treat inflammatory and autoimmune diseases  
 CC such as rheumatoid arthritis, inflammatory bowel disease,  
 CC graft-versus-host disease, diabetes, psoriasis and Graves' disease.  
 CC Infectious diseases such as HIV-induced lymphopenia, fulminant viral  
 CC hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated  
 CC ulceration, ischaemia and reperfusion conditions including acute  
 CC myocardial infarction, acute coronary syndrome, congestive heart failure  
 CC and atherosclerosis, and Alzheimer's and Parkinson's diseases, acute lung  
 CC injury and acute respiratory distress syndrome, Crohn's disease, brain  
 CC trauma and injury, chronic glomerulonephritis, osteoporosis, aplastic  
 CC anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and  
 CC multiple sclerosis. In addition, the gene and protein can be used to  
 CC prevent apoptosis following organ transplantation.  
 XX  
 SQ Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;

## Alignment Scores:

Pred. No.: 3.85e-77 Length: 900  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-936-024-1 (1-271) x AAA53208 (1-900)

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 Db 88 GTGGCAGAAACACCCACCTTACCCCTGGCGGGACGAGAGAGGGGAGCGGTGGTGTGC 147  
 Qy 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40  
 Db 148 GCCAGTGGCCCCCAGGACCTTTGTGCAGCGCGCTGCCCGCGAGACAGCCCCAGCAGC 207  
 Qy 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60  
 Db 208 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACTGTGAGCGCTGCCGC 267  
 Qy 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80  
 Db 268 TACTCAACGTCCTCTGGGGGAGCGTGAGGAGGGGACCGGGCTTGGCCACCCACCCAC 327  
 Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
 Db 328 AACCGTGCTGCGCTGCCGACCGGCTTCTTCGCGACGCTGGTTCTGTCTTGGAGCAC 387  
 Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120  
 Db 388 GCATCGTGTCCACCTGTGTCGGCGGTGATTGCCCGGGGACCCCGCCAGCAGCAACACG 447  
 Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140  
 Db 448 TGCCAGCGCTGCCCGCCCGGACCTTCTCAGCCAGCAGCTCCAGCTCAGCAGGTGCCAG 507  
 Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160  
 Db 508 CCCACCGCAACTGCACGGCCCTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 567  
 Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
 Db 568 GACACCTGTGCACCACTGCAGGCTTCCCTCCCTCAGCACCAGGTTACCGAGGTGAG 627  
 Qy 181 GluCyGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLeuArgLeu 200



Dh 628 GAGGTGAGCGTCCGTCATGACTTGTGCTTCCAGACATCTCCATCAAGAGCGTG 687  
Qy 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGlnGlyTTPGlyProThrProArgAlaGly 220  
Dh 688 CAGGGCGTGTGAGCGCTCGAGGCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGC 747  
Qy 221 ArgAlaAlaLeuGlnLeuLeuLeuArgArgArgLeuThrGlnLeuLeuGlyAlaGlnAsp 240  
Dh 748 CGCGCGCTTGCAGCTGAGCTCGTGCAGCTCAAGAGCTCTTGGGGCGCAGGAC 807  
Qy 241 GlnAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGln 260  
Dh 808 GGGCGCTGTGCTGGCGCTGCTGAGCGCTGCGCTGCGCAGAGTCCCGGCTGGAG 867  
Qy 261 ArgSerValArgGlnArgPheLeuProValHis 271  
Dh 868 CGAGCGCTTCCGTGAGCGCTTCTCTCTGTGCAC 900  
RESULT 9  
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ID AAAS1075 standard; DNA; 900 BP.  
XX  
AC AAAS1075;  
DT 26-SEP-2000 (first entry)  
XX  
DE Human FLINT coding sequence.  
XX  
FLINT, osteoprotegerin 3; OPG3, tumour necrosis factor receptor, TNFR;  
Kw FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;  
Kw anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;  
Kw anti-inflammatory; antibacterial; immunosuppressive; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..900  
FT /\*tag= a  
FT /product= FLINT  
FT /partial  
FT sig\_peptide 1..87  
FT /\*tag= b  
FT mat\_peptide 88..900  
FT /\*tag= c  
XX  
PN MO200037094-A2.  
XX  
XX 29-JUN-2000.  
XX  
XX 21-DEC-1999; 99WO-US30734.  
XX  
XX 22-DEC-1998; 98US-0113407.  
XX 30-MAR-1999; 99WO-US06797.  
XX 20-OCT-1999; 99US-0172239.  
XX  
XX (ELIL ) LILLY & CO ELI.  
XX  
XX Cohen FJ, Posada JA, Wierda D;  
XX  
XX MPI; 2000-475441/41.  
XX P-PSDB; AAY96596.  
XX  
XX Use of mature FLINT for treating e.g. acute respiratory distress  
XX syndrome, ulcerative colitis or ischemic injury during organ  
XX transplantation  
XX  
XX Example 7, Fig 1A-B; 125pp; English.  
XX  
XX Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis  
XX factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and  
XX prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas  
XX mediated apoptotic and pro-inflammatory activity. mFLINT is useful for  
XX treating acute respiratory distress syndrome, treating or inhibiting

CC ulcerative colitis, inhibiting ischemic injury during organ  
CC transplantation or for organ preservation during transplantation. mFLINT  
CC can also be used to treat acute liver failure, inflammation of the liver,  
CC abnormal (hepatocyte) apoptosis, sepsis, disorders associated with  
CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,  
CC damage to a cardiac myocyte resulting from abnormal myocardial ischemia,  
CC Type I diabetes, cancer, damage to an innocent bystander tissue induced  
CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,  
CC myelodysplastic syndromes and pancytopenic conditions.  
XX  
SQ Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other:  
Alignment Scores:  
Pred. No.: 3.85e-77 Length: 900  
Score: 1491.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0  
US-09-936-024-1 (1-271) x AAAS1075 (1-900)  
Qy 1 ValAlaGlnThrProThrTyrProTyrArgAspAlaGlnThrGlyGlnArgLeuValCys 20  
Dh 88 GTGGCAGAAACACCCACCTACCTCTGGGGGACCGCAGACAGGAGCGGCTGTGTGC 147  
Qy 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40  
Dh 148 GCCAGTGCCTCCCGGACCTTTGTGACGGCGGCTGCCCCGACAGACAGCCACGACG 207  
Qy 41 CysGlyProCysProProArgHisTyrThrGlnPheThrPheValTyrLeuGlnArgCysArg 60  
Dh 208 TGTGGCCCGTGTCCACCGCGCCCACTACACCGAGTTCTGGAATCACTGGAGCGTGC 267  
Qy 61 TyrCysAsnValLeuCysGlyGlnArgGlnGlnAlaArgAlaCysHisAlaThrHis 80  
Dh 268 TACTGCAACGTCCTCTGTGGGGAGCGTGGAGAGGACCGGCTTGGCACGCCACCCAC 327  
Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHis 100  
Dh 328 AACGTCCTGCGCTGCGGACCGGCTTCTTGGCAGCGTGGTTTGTGTGAGACAC 387  
Qy 101 AlaSerCysProProGlyAlaGlyValAlaLeuProGlyThrProSerGlnAsnThrGln 120  
Dh 388 GCATCGTGTCCACCTGGTGGCGGGGTATGTCGCCGGGACCCCGACGACCAACACGCG 447  
Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGlnCysGln 140  
Dh 448 TGCCAGCGTGCCTCCCGGACCGCTTCAAGCAGACGCTTCAAGCAGAGCTGCGAG 507  
Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160  
Dh 508 CCCACCGCAACTGACAGCGCTTGGGCTGCTCAATGTGCCAGGCTCTTCTCCCAT 567  
Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGln 180  
Dh 568 GACACCTGTGTCAACAGTGTGACTGCTTCCCTTCAAGCAGACAGGATACAGAGCTGAG 627  
Qy 181 GlnCysGlnArgAlaValAlaAspPheValAlaPheGlnAspIleSerIleLeuArgLeu 200  
Dh 628 GAGTGTGAGCTGCGCTGTCATGACCTTGTGTGCTTCCAGGACATCTCATCAAGAGCTG 687  
Qy 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGlnGlyTTPGlyProThrProArgAlaGly 220  
Dh 688 CAGCGCTGTGAGCGCTTGCAGGCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGC 747  
Qy 221 ArgAlaAlaLeuGlnLeuLeuLeuArgArgArgLeuThrGlnLeuLeuGlyAlaGlnAsp 240  
Dh 748 CGCGCGCTTGCAGCTGAGCTCGTGCAGCTCAAGAGCTCTTGGGGCGCAGGAC 807  
Qy 241 GlnAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGln 260  
Dh 808 GGGCGCTGTGCTGGCGCTGCTGAGCGCTGCGCGTGGCAGAGATGCCGGGCTGGAG 867

QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
 Db 868 CGAGCGGTCGTCGAGCGCTTCCTCCCTGTGCAC 900

## RESULT 10

AAAX22300  
 ID AAX22300 standard; DNA; 903 BP.

AC AAX22300;

DT 20-MAY-1999 (first entry)

XX Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.

XX HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;  
 KW tumour necrosis factor receptor; muscle disorder; bone mass; screening;  
 KW muscle metabolism; binding agent; cognate ligand; ss.

XX Homo sapiens.

XX WO9907738-A2.

XX 18-FEB-1999.

XX 04-AUG-1998; 98WO-US16202.

XX 06-AUG-1997; 97US-0054869.

XX (PROC ) PROCTER & GAMBLE CO.

XX (REG-) REGENERON PHARM INC.

XX Mastakowski PJ, Morris J, Valenzuela DM;

XX WPI; 1999-167365/14.

XX P-PSDB; AAW95082.

XX Novel orphan human receptor polypeptide and nucleic acid - useful as  
 PT diagnostic reagents and for treatment of muscle disorders

XX Claim 2; Page 21; 23pp; English.

XX This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The  
 CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor  
 CC receptor (TNFR). Host cells transformed with a vector comprising the  
 CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the  
 CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the  
 CC protein are useful for diagnosis and treatment of humans and animals,  
 CC especially muscle disorders, as the receptor is involved in regulation of  
 CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful  
 CC for screening for novel binding agents, and cognate ligands, which may be  
 CC used to treat disorders associated with HUMAN NTR-1 imbalance.

XX Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;

## Alignment Scores:

Pred. No.: 3,86e-77 Length: 903  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0

US-09-936-024-1 (1-271) x AAX22300 (1-903)

QY 1 ValAlaGluThrProThrTyrProThrArgAspAlaGluThrGlyGluArgLeuValCys 20  
 Db 88 GTGGCGAAACACCCACTACCTCCCTGGCGGAGCGAGACAGCGGCGGTGGTGC 147

QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40  
 Db 148 GCCCAGTGGCCCGCCAGGCACCTTTGTGACGGCGCGTGGCCGCGAGACAGCCCGACGAGC 207

QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrIleuGluArgCysArg 60  
 Db 208 TGTGGCCCGTGTCCACCGCGCCACTACACGCGAGTTCTGGAACTACTGTGAGCGCTGCCGC 267  
 QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaAtrGAlaCysHisAlaThrHis 80  
 Db 268 TACTGCACGTCCTCTGCGGGAGCGTGAGGAGGAGGACCGGGCTTGCACGCCACCCAC 327  
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
 Db 328 AACCGTGCCTGCCGCGCACCGGCTTCTTCGCGCAGCGTGGTTCTCTGCTTGAGGAC 387  
 QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120  
 Db 388 GCATCGTGTCCACCTGTGCGCGCGTGTTCGCCGGGACCCGCCAGCAGACACGCGAG 447  
 QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSerSer 140  
 Db 448 TGCCAGCGCTGCCCGCCAGGCACCTTCTCAGCCAGAGCTCCAGCTCAGAGCAGTGCCAG 507  
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160  
 Db 508 CCCACCGCAACTGCAACGCGCTGGGCGCTGCGCCCTCAATGTGCCAGGCTCTTCTCCCAT 567  
 QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
 Db 568 GACACCTGTGCACAGCTGCACCTGGCTTCCCGCTCAGCACAGGCTACAGAGGTGAG 627  
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleValArgLeu 200  
 Db 628 GAGTGTGAGCGTGGCGTCAATCGACTTTTGGCTTTCCAGGACATCTCCATCAAGAGGTG 687  
 QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220  
 Db 688 CAGCGGCTGTGCAGGCGCTCGAGGCGCGGAGGCGGTCCGACACACAGGCGGCG 747  
 QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240  
 Db 748 CGCGCGGCTTGTGAGCTGAAGCTGCGTGGCGGCTCAGCGAGCTCTCTGGGGCGCGAGGAC 807  
 QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaAlaArgMetProGlyLeuGlu 260  
 Db 808 GGGGCGCTCTGTGGCGGTGTGCGAGGCGCTGCGCGGTGGCCAGGATGCCGGGCTGGAG 867  
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
 Db 868 CGAGGCTCCGTGAGGCGCTTCTCTCCCTGTGCAC 900

## RESULT 11

AAAD3295

ID AAD3295 standard; DNA; 903 BP.

XX AAD3295;

XX 01-JUL-2002 (first entry)

XX Mammalian synthetic tumour necrosis factor receptor (TNFR)-6alpha DNA.  
 DE Tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;  
 KW immune system-related disorder; inflammatory disease; immunosuppressive;  
 KW bowel disease; encephalitis; atherosclerosis; gastrointestinal-gen;  
 KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;  
 KW multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;  
 KW graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;  
 KW neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor;  
 KW gene; ds.

XX Mammalia.

OS Synthetic.

XX WO200218622-A2.

XX 07-MAR-2002.

PD

XX 24-AUG-2001; 2001WO-US26396.  
 PF 25-AUG-2000; 2000US-227598P.  
 XX 21-NOV-2000; 2000US-252131P.  
 PR 06-JUL-2001; 2001US-303224P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Gentz RL, Edner R, Yu G, Ruben SM, Ni J, Feng P;  
 XX WPI; 2002-281068/32.  
 DR  
 XX Novel nucleic acid molecules comprising a polynucleotide encoding human  
 PT tumor necrosis factor receptor (TNFR)-galpha and 6beta polypeptides  
 PT useful for treating disease e.g. inflammatory and autoimmune disorders  
 PT  
 XX Claim 37; Page 348; 350pp; English.  
 XX  
 XX The invention relates to human tumour necrosis factor receptor (TNFR) -  
 CC 6alpha and 6beta protein and their corresponding nucleic acids. The  
 CC invention provides screening methods for identifying agonists and  
 CC antagonists of TNFR-6alpha and 6beta activity. The invention also  
 CC provides diagnostic and therapeutic methods for detecting and treating  
 CC immune system-related disorders. The method is useful for treating or  
 CC preventing an inflammatory disease or disorder selected from bowel  
 CC disease, enterocolitis, atherosclerosis and psoriasis, an autoimmune  
 CC disease or disorder selected from systemic lupus erythematosus,  
 CC arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,  
 CC and autoimmune encephalitis, graft versus host disease (GVHD), and an  
 CC allergy or asthma. The present sequence is Mammalian synthetic TNFR-  
 CC 6alpha DNA.  
 XX  
 SQ Sequence 903 BP; 171 A; 253 C; 265 G; 214 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3.86e-77 Length: 903  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-936-024-1 (1-271) x AAD33295 (1-903)  
 QY 1 ValAlaGluThrProThrTyrProTyrArgAspAlaGluThrGlyGluArgLeuValCys 20  
 DB 88 GTGGCTGAAACACCTACATATCCATGAGAGATGCTGAAACAGGAAAGGCTGTGTGT 147  
 QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40  
 DB 148 GCTAGTGTCTCTCTGGAACATTTGTGCAAGGCTGTAGCGGATTCCTTACGACG 207  
 QY 41 CysGlyProCysProProArgHisTyrThrGlnPheThrPasnTyrLeuGluArgCysArg 60  
 DB 208 TGTGGCCCTTGCTCTGAGCACTATPACACAGTTTGAATCTCTGACCGCTGAGG 267  
 QY 61 TyrCysAsnValLeuGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80  
 DB 268 TATTCACACGCTCTCTGGAGAAAGGAGAGAGCAAGCGCTGTTCATGCAACACAC 327  
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
 DB 328 AACAGGGGATGTAGGTGTGCGACAGGCTTCTTGTCTCATGTGGAATTTTGTCTGAAACAC 387  
 QY 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120  
 DB 388 GCTTCTTGTCTCTCTGGGTGGAGTATGCTCTGTTACACCTCTCAACAACACCA 447  
 QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140  
 DB 448 TGCAGGCTGTCTCTCTGGGACCTTCTCTGATCTAGCTCAGCTCTGAAACAATGCGAA 507

QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160  
 DB 508 CTTACCGGCATTTTACAGCTCTGGAGCTGGCTCTGAAACGCTGTGTTCTCTCCAT 567  
 QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
 DB 568 GATACCTGTGTACAAAGCTGTAAGGCTTCTCTCTCTACCCGCGTGGCGCTGAA 627  
 QY 181 GlucyGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleValArgLeu 200  
 DB 628 GAGTGCACAGCGCTGTGATGACTTGTGCTTCCAGGATATCTATCAAAAGGCTG 687  
 QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220  
 DB 688 CAAGCGCTGCTGCAAGCTCTGGAAGCTCTGAGGGCTGGGCTCCACACCAAGGCTGGC 747  
 QY 221 ArgAlaAlaLeuGlnLeuValLeuArgArgArgLeuThrGluLeuGlyAlaGlnAsp 240  
 DB 748 AGGCTGCTGCTGCAACTGAAAGCTTCGACAGAGGCTCACTGAACCTCTGGAGCTCAAGAT 807  
 QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260  
 DB 808 GGAAGCTGTGCTGTGAGAGCTGTGCAAGCTCTGAGGGTGGCAAGATGCTTGAAGCTGAG 867  
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
 DB 868 CGCTCTGAGGAGAACGCTTCTCTGCTGTCAC 900  
 RESULT 12  
 ID AAF62705  
 AAFA62705 standard; cDNA; 1055 BP.  
 XX  
 AC AAF62705;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Human NTR3 nucleotide sequence.  
 XX  
 KW Human; NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;  
 KW antianaemic; immunosuppressive; antidiabetic; antiviral; antibacterial;  
 KW cytoskeletal; neuroprotective; antiinflammatory; anorectic; vasotropic;  
 KW antitumour; antiarthritic; cerebroprotective; tuberculostatic;  
 KW gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;  
 KW infection; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX MO200110908-A1.  
 PN  
 XX PD 15-FEB-2001.  
 XX  
 XX 02-AUG-2000; 2000WO-US21287.  
 PF  
 XX 04-AUG-1999; 99US-0147297.  
 PR  
 XX (AMGE-) AMGEN INC.  
 PA  
 XX Heu H;  
 PT  
 XX WPI; 2001-191521/19.  
 DR P-PSDB; AAB71754.  
 PT New tumor necrosis factor receptor, NTR3, useful for treating cancers,  
 PT stroke, anemia, obesity, rheumatoid arthritis and transplantation  
 PT rejection -  
 PT  
 XX Claim 1; Page 128-129; 135pp; English.  
 XX  
 XX The present sequence encodes the tumour necrosis factor (TNF) receptor  
 CC polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful  
 CC for treating diseases such as acquired-immunodeficiency syndrome (AIDS),  
 CC anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,

CC diabetes mellitus, disseminated intravascular coagulopathy, erythroid  
 CC sick syndrome, haemorrhagic shock, hepatitis, insulin resistance.  
 CC leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,  
 CC obesity, rejection of transplanted organs, rheumatoid arthritis, septic  
 CC shock syndrome, stroke, adult respiratory distress syndrome (ARDS),  
 CC tuberculosis, and a number of viral diseases. The NTR3 polypeptide is  
 CC useful for identifying or developing new (ant)agonists of NTR3. It may  
 CC be used as an immunogen to which antibodies may be raised. NTR3 nucleic  
 CC acid molecules may be useful as hybridisation probes in diagnostic assays  
 CC to test, either qualitatively or quantitatively, for the presence of an  
 CC NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid  
 CC samples.  
 XX

SQ Sequence 1055 BP; 160 A; 369 C; 340 G; 186 T; 0 other;

## Alignment Scores:

Pred. No.: 4 54e-77 Length: 1055  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-09-936-024-1 (1-271) x AAF62705 (1-1055)

QY 1 ValAlaGluThrProThrTyProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20  
 Db 154 GTGGAGAAACACCCACTACCTCCCTGGCGGACGACAGACAGGGAGCGCTGGTGTGC 213  
 QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgSerProThrThr 40  
 Db 214 GCCAGTGCCTCCCGCAGCACCTTTGTGCAGCGCGGTGGCGGACAGACAGCCACGACG 273  
 QY 41 CysGlyProCysProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60  
 Db 274 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACTCTGGAGCGCTGCCGC 333  
 QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaAlaArgAlaCysHisAlaThrHis 80  
 Db 334 TACTGCAACCTCTCTGCGGGGAGCGTGAGGAGGAGCAGCGGCTTGCCACAGCCACCCAC 393  
 QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
 Db 394 AACCGTCCCTGCGCGTCCCGCACCGGCTTCTTCGCGCACGCTGGTTCTGCTTGGAGCAC 453  
 QY 101 AlaserCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120  
 Db 454 GCATCGTGTCCACTGTGTGCGCGGTGATTGCCCCGGGACCCCGCCAGCCAGAACAGCGAG 513  
 QY 121 CysGlnProCysProGlyThrPheSerAlaserSerSerSerGluGlnCysGln 140  
 Db 514 TGCCAGCGTGCCTCCCGCAGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 573  
 QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160  
 Db 574 CCCACCGCAACTGCACGCGCCCTGGGCGCTGCGCCCTCAATGTGCAGGCTCTTCTCCCAT 633  
 QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
 Db 634 GACACCTGTGCACCACTGCATCTGGCTTCCCTCTGACACAGGGTACAGAGCTGAG 693  
 QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200  
 Db 694 GAGTGTGAGCGTGCCTCATCGACTTGTGGCTTTCAGGACATCTCCATCAAGAGCGTG 753  
 QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220  
 Db 754 CAGCGGTGTGTGAGGCGCTCGAGCGCCCGGAGGCGTGGGGTCCGACACCAAGCGCGGC 813  
 QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240  
 Db 814 CGCGCGGCTTGCAGCTGAAGCTGCTGCGGCGCTCAGGAGCTCTTGGGGGCGCAGGAC 873

QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260  
 Db 874 GGGGGCGCTGCTGGTGGCGGTCTGTCAGGCGCTGCGGTGGCCAGGATGCCGGGCTGGAG 933  
 QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
 Db 934 CGGAGCGTCCGTGAGCGCTTCTCTCCCTGTGCAC 966  
 RESULT 13  
 AAAS3802  
 ID AAAS3802 standard; cDNA; 1066 BP.  
 XX  
 AC AAAS3802;  
 XX  
 DT 19-DEC-2000 (first entry)  
 XX  
 DE M68 TNF receptor related protein coding sequence.  
 XX  
 KW M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;  
 KW receptor; immune response; cell differentiation; ligand; cancer;  
 KW bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;  
 KW Grave's disease; idiopathic myxedema; autoimmune diabetes;  
 KW thrombotic thrombocytopenic purpura; multiple sclerosis;  
 KW liver diseases; autoimmune gastritis; ulcerative colitis;  
 KW glomerulonephritis; pulmonary fibrosis; heart failure;  
 KW atherosclerosis; aplastic anaemia; myelodysplastic syndromes;  
 KW osteoporosis; Alzheimers disease; parkinsons disease; stroke;  
 KW myocardial infarction; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 53..955  
 FT /tag= a  
 FT /product= M68 polypeptide  
 XX  
 FN WO200046247-A1.  
 XX  
 PD 10-AUG-2000.  
 XX  
 PF 04-FEB-2000; 2000WO-US03037.  
 XX  
 PR 05-FEB-1999; 99US-0118902.  
 PR 20-DEC-1999; 99US-0172754.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Bai C;  
 XX  
 DR WPI; 2000-506066/45.  
 DR P-PSDB; AAY97246.  
 XX  
 PT Isolated human M68 nucleic acids and proteins which are part of the  
 PT tumor necrosis factor receptor (TNFR) family, useful for identifying  
 PT modulators that may be used to treat various diseases e.g. cancer,  
 PT osteoporosis, Alzheimer's disease  
 XX  
 PS Claim 21; Page 73-75; 80pp; English.  
 XX  
 CC The M68 protein is a member of a family of proteins which have  
 CC roles in immune responses, cell death, cell proliferation and  
 CC stimulation of cell differentiation. M68 lacks a transmembrane domain  
 CC and is a secreted factor suggesting that it functions as a natural  
 CC inhibitor for its ligand. The altered expression pattern of M68 in a  
 CC multitude of tissues suggests that M68 may play a role in cancer by  
 CC binding to its ligand and blocking apoptotic cell death induced by  
 CC such a ligand. This anti-apoptotic role of M68 suggests that  
 CC modulators of M68 will be useful in treatment of apoptosis-related  
 CC diseases such as various forms of cancer and various bone disorders.  
 CC M68 nucleic acids and proteins are therefore useful for treating  
 CC conditions involving atypical apoptosis and for identifying  
 CC modulators of M68. Modulators of M68 are useful for treatment of  
 CC cancer and other diseases associated with abnormal levels of

CC apoptosis including systemic lupus erythematosus, Hashimoto's  
 CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune  
 CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,  
 CC liver diseases, autoimmune gastritis, ulcerative colitis,  
 CC glomerulonephritis, pulmonary fibrosis, heart failure,  
 CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,  
 CC osteoporosis, Alzheimer's disease, Parkinson's disease, stroke, and  
 CC myocardial infarction.

XX  
 XX  
 SQ Sequence 1066 BP; 178 A; 367 C; 335 G; 186 T; 0 other;

Alignment Scores:  
 Pred. No.: 4.59e-77 Length: 1066  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0

US-09-936-024-1 (1-271) x AAAS3802 (1-1066)

Qy 1 ValAlaGluThrProThrTyProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20  
 Db 140 GTGCGAAGAACACCACTACCCCTGGGGAGCGAGAGACAGGAGCGGCTGTGTGC 199

Qy 21 AlaGlnCysProProGlyLysThrPheValGlnArgProCysArgAspSerProThrThr 40  
 Db 200 GCCCAGTGCCCGCCAGGACCTTTGTGAGCGCGCTGCCCGCCAGACGCCACGACG 259

Qy 41 CysGlyProCysProProArgHisLysThrGlnPheTrpAsnTyLysGluArgCysArg 60  
 Db 260 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCGAACTCGAAGCGCTGCGCGC 319

Qy 61 TyrCysAsnValLysCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80  
 Db 320 TACTGCAACGCTCTGTGGGAGCGTGAAGAGAGAGAGCGGCTTGCACAGCCAC 379

Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
 Db 380 AACGTCCTGCGCGCTCCGCGACCGGCTCTCCGCGACCGTGTGTTGTGGAGCAC 439

Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyLysProSerGlnAsnThrGln 120  
 Db 440 GCATCGTGTCCACTGTGTGCGCGGTATTCGCCGCGACCCCGACAGACAGCAG 499

Qy 121 CysGlnProCysProProGlyLysThrPheSerLysSerSerSerSerGluGlnCysGln 140  
 Db 500 TGCACGCGTGTCCCGCCAGGACCTTCTCACAGCAGCACTCAGACAGACGTGCCAG 559

Qy 141 ProHisArgAsnCysThrAlaLeuGlyLysAlaLeuAsnValProGlySerSerSerHis 160  
 Db 560 CCCACCGCAACCTCAGCGCGCTGGGCTGGCCCTCAATGTGCCAGGCTCTTCCAT 619

Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
 Db 620 GACACCTGTGCAACACTGCACTGGCTTCCCTCAGACACAGAGTACAGAGCTGAG 679

Qy 181 GlnCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200  
 Db 680 GAGGTAGGCTGCGTGCATCTGCTTGTGCTTCCAGGACATCTCATMAAGGCTG 739

Qy 201 GlnArgLeuGlnAlaLeuGluAlaProGluGlyLysProGlyProThrProArgAlaGly 220  
 Db 740 CAGCGGCTGTGCGAGCGCTCGAGGCCCGAGGCTGGGGTCCGACACCAAGGCGGCG 799

Qy 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuGlyAlaGlnAsp 240  
 Db 800 CGCGCGGCTTGTGAGCTGAGCTGCTGTGCGGCTCAGGAGCTCTGTGGGCGCCAGAC 859

Qy 241 GlnAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLysGlu 260  
 Db 860 GGGCGCTGTGTGTGCGGCTGTGCGAGCGCTGCGCGTGGCCAGAGATGCCGGGCTGAG 919

Qy 261 ArgSerValArgGluArgPheLeuProValHis 271  
 Db 920 CGAGCGCTCGGTGAGCGCTTCTCTCCCTGTGCAC 952

RESULT 14  
 AAV39085  
 ID AAV39085 standard; cDNA; 1077 BP.  
 XX  
 AC AAV39085;  
 XX  
 DT 26-OCT-1998 (first entry)  
 XX  
 DE Human tumour necrosis factor receptor-6 alpha cDNA.  
 XX  
 KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;  
 KW endothelial cells; keratinocytes; normal prostate; apoptosis;  
 KW prostate tumour tissue; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 25..927  
 FT /\*tag= a  
 FT /product= "TNFR-6 alpha protein"  
 FT sig\_peptide 25..114  
 FT /\*tag= b  
 FT mat\_peptide 115..924  
 FT /\*tag= c

XX  
 PN WO9830694-A2.  
 XX  
 PD 16-JUL-1998.  
 XX  
 PF 13-JAN-1998; 98MO-US00153.  
 XX  
 PR 14-JAN-1997; 97US-0035496.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ehner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;  
 XX  
 DR WPI; 1998-399142/34.  
 DR P-PSDB; AAW63622.  
 XX  
 PT Human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
 PT the diagnosis of immune system-related disorder(s)  
 XX  
 PS Disclosure; Fig 1; 91pp; English.  
 XX

CC The present sequence represents the human tumour necrosis factor  
 CC receptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides  
 CC for the TNFR-6 beta cDNA (AAV39086). TNFR-6 alpha and TNFR-6 beta are  
 CC members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
 CC are expressed in endothelial cells, keratinocytes, normal prostate and  
 CC prostate tumour tissue. For a number of disorders of these cells,  
 CC particularly of the immune system, substantially altered (whether  
 CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene  
 CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta  
 CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
 CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
 CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are  
 CC also claimed to be useful for identifying ligands which may be useful  
 CC in the treatment of apoptosis related disorders.

XX  
 SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

Alignment Scores:  
 Pred. No.: 4.64e-77 Length: 1077  
 Score: 1491.00 Matches: 271  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0

US-09-936-024-1 (1-271) x AAV39085 (1-1077)

Qy 1 ValAlaGluThrProThrTyProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20  
Db 112 GTGGCAGAACACCCACCTTGTGCAGCGCGCTGGCGGACGCAGACAGCGGCGCTGGTGTGC 171

Qy 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40  
Db 172 GCCCAGTCCCGCCAGCACCTTGTGCAGCGCGCTGGCGGACGCAGACAGCGGCGCTGGTGTGC 231

Qy 41 CysGlyProCysProArgHisTyThrGlnPheTrpAsnTyRleuGluArgCysArg 60  
Db 232 TGTGGCGCGTGTCCACCGCGCCACTACAGCAGTTCTTGGAACTTACCTGGAGCGCTCCCGC 291

Qy 61 TyCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80  
Db 292 TACTGCAACGTCTCTGGGGAGCGTGAGGAGGAGCAGCGGCTTGGCCAGCCACCCAC 351

Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
Db 352 AACCGTGCCTCGCGCTGCCACCGCGCTTCTTCGCGCAGCGCTGTTCTGCTTGGAGCAC 411

Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120  
Db 412 GCATCGTGTCCACCTGGTGCAGCGCGTATTTGCCCGCGCACCCCGGAGCAGACGCGAG 471

Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140  
Db 472 TGCAGCGCGTGCCTCCCGCAGCACCTTCTCAGCCAGCAGCTCCAGCTCAGACGAGTCCGAG 531

Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160  
Db 532 CCCACCGCAACTGCACGGCGCTGGCGCTGGCGCTCAATGTGCAGGCTCTTCTCCCAT 591

Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180  
Db 592 GACACCTGTGCACCACTGCATCGGCTTCCCGCTCAGCACCGGCTACCGAGGCTGAG 651

Qy 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200  
Db 652 GAGTGTGAGCGTCCGCTCATCGACTTGTGGCTTTCAGGACATCTCCATCAGAGGCTG 711

Qy 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrpGlyProThrProArgAlaGly 220  
Db 712 CAGCGGCTGTGCAGGCGCTCGAGGCGCCCGAGGGCTGGGGTCCGACACCAAGGGCGGC 771

Qy 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrCluLeuLeuGlyAlaGlnAsp 240  
Db 772 CGCGCGGCTTGCAGCTGAAGCTGCGTCCGCGGCTCAGCGAGCTCTCGGGGCGCAGGAC 831

Qy 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260  
Db 832 GGGCGCTGTGTGGCTGTGCTGTGCAGGCGCTGGCGTGGCCAGGATGCCCGGCGCTGGAG 891

Qy 261 ArgSerValArgGluArgPheLeuProValHis 271  
Db 892 CGGAGCGTCCGTGAGCGCTTCTCCCTCGCTGTGCAC 924

## RESULT 15

AAA37772  
ID AAA37772 standard; DNA; 1077 BP.

XX

AC AAA37772;

XX

DT 04-DEC-2000 (first entry)

XX

DE Human tumour necrosis factor receptor-6 alpha coding sequence.

XX

KW Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;  
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;  
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;  
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;

KW thyroid associated ophthalmopathy; cell damage; parasitic infection;  
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;  
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;  
KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;  
KW psoriasis; septic shock; ulcerative colitis; therapy; ds.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 25..927  
FT /\*tag= a  
FT /product= TNFR-6alpha

XX WO200052028-A1.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000WO-US05686.

XX 04-MAR-1999; 99US-0121774.

PR 12-MAR-1999; 99US-0124092.

PR 27-APR-1999; 99US-0131279.

PR 30-APR-1999; 99US-0131964.

PR 02-AUG-1999; 99US-0146371.

PR 01-DEC-1999; 99US-0168235.

XX (HUMA-) HUMAN GENOME SCI INC.

XX

XX Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;

XX WPI: 2000-572174/53.

DR P-PSDB; AAY90357.

XX

PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)  
PT proteins TNFR-6alpha and TNFR-6beta, useful for treating e.g.  
PT Alzheimer's disease, osteoporosis and graft rejection -

XX

XX Claim 2; Fig 1; 332pp; English.

XX

CC This sequence encodes the human tumour necrosis factor receptor 6  
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
CC and protein sequences can be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate TNFR expression. The  
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against  
CC them may be used for the treatment of a range of conditions such as  
CC disorders associated with neovascularisation (especially ocular  
CC neovascularisation) (such as solid tumours and malignancies (e.g.  
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
CC and pre-maturity macular degeneration), allergies, inflammation, microbial  
CC thyroid associated ophthalmopathy tissue/cell damage, wounds, microbial  
CC and parasitic infections, bone disease (e.g. osteoporosis),  
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
CC disorders (e.g. graft rejection), rheumatism, liver disease,  
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
CC colitis.

XX Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;

SQ

## Alignment Scores:

Pred. No.:	4,64e-77	Length:	1077
Score:	1491.00	Matches:	271
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-936-024-1 (1-271) x AAA37772 (1-1077)

Qy 1 ValAlaGluThrProThrTyProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20

Db 112 GTGGCAGAACACCCACCTTACCCCTGGCGGACGCAGACAGCGGCGCTGGTGTGC 171

```
Qy 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgAspSerProThrThr 40
Db 172 GCCAGTGCCTCCCGAGGACCTTTGTGAGCGGCGGTGCCGCGAGACAGCCCGCAGACG 231
Qy 41 CysGlyProCysProProArgHisTyrThrGlnPheTyrPheTyrLeuGlnArgCysArg 60
Db 232 TGTGGCCGTTGTCACCGCGGCTACACGCGATTCTGGAACTACTGGAGCGGTGCGC 291
Qy 61 TyrCysAsnValLeuCysGlyGlyArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 292 TACTGCAAGCTCTCTGAGGAGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 351
Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysAlaGlnHis 100
Db 352 AACCGTGCCTCCGCTGCGGACCGGCTTCTTCCGCGACGCTGGTTCTGCTTGAGAC 411
Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 412 GCATCGTGTCCACCTGGTGCCTGGGCTGATTGCCCGGCGACCCCGAGCCAGMACACG 471
Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSer 140
Db 472 TGCCAGCCGTCGCCCCGAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGACAGTGCAG 531
Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
Db 532 CCCACCGCAACTGCAAGGCTTGGGCTTGGCTTCAATGTCAGGCTTCTTCCCAT 591
Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGln 180
Db 592 GACACCTGTGACACGAGTGCATGCTTCCCTCAGCACGAGGTACGAGGAGCTGAG 651
Qy 181 GluCysGlnArgAlaValIleAspPheValAlaPheGlnAspIleSerIleValArgLeu 200
Db 652 GAGTGTGAGCGTCGCTCATGACTTTGTGGCTTTCCAGACATCTCCATCAAGAGGCTG 711
Qy 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGlnGlyTyrGlyProThrProArgAlaGly 220
Db 712 CAGCGGCTGCTGCAAGGCTTGAAGGCTTGGGCTTGGGCTTGGGCTTGGGCTTGGGCT 771
Qy 221 ArgAlaAlaLeuGlnLeuValLeuArgArgArgLeuThrGlnLeuGlyAlaGlnAsp 240
Db 772 CGCCGCGCTTGCAGCTGAACTGCTGCGCGGCTCAGGAGCTCTGCGGCGCAGGAGC 831
Qy 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGln 260
Db 832 GGGCGGCTGCTGTGCGGCTGCTGAGGCGCTGCGCGCTGCGCGAGATGCCGCGCTGAG 891
Qy 261 ArgSerValArgGlnArgPheLeuProValHis 271
Db 892 CGGAGCGTCCCTGAGCGCTTCTCTCTGTGCAC 924
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Job time : 236 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:32 ; Search time 21 Seconds  
(without alignments)  
535,242 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491  
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARMGELRSYERELPVH 271

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	100.0	300	1 TR6B_HUMAN	O95407 homo sapien
2	440.5	29.5	401	1 T11B_HUMAN	O00300 homo sapien
3	425.5	28.5	401	1 T11B_RAT	O08727 rattus norv
4	424.5	28.5	401	1 T11B_MOUSE	O08712 mus musculu
5	340.5	22.8	461	1 TR1B_HUMAN	P20333 homo sapien
6	332.5	22.1	474	1 TR1B_MOUSE	P25119 mus musculu
7	299.5	20.1	435	1 TRN3_HUMAN	P36941 homo sapien
8	288.5	19.3	655	1 TRN2_MOUSE	O9509 mus musculu
9	287	19.2	655	1 TRN1_HUMAN	O75509 homo sapien
10	265.5	17.8	445	1 TRN3_MOUSE	P50284 mus musculu
11	260	17.4	349	1 CRMB_VARV	P34015 variola vir
12	257.5	17.3	349	1 CRMB_CAMPS	O8uyat camelpox vi
13	254.5	17.1	351	1 CRMB_COMX	O73559 cowpox viru
14	244	16.4	283	1 TR1A_HUMAN	O92956 homo sapien
15	235.5	15.8	616	1 TR1I_MOUSE	O9y666 homo sapien
16	234.5	15.7	325	1 VT2_SPKVA	P25943 shope fibro
17	220.5	14.8	625	1 TR1I_MOUSE	O35305 mus musculu
18	215.5	14.5	277	1 TRN4_HUMAN	P43469 homo sapien
19	211.5	14.2	277	1 TRN4_RAT	P15725 rattus norv
20	210.5	14.1	277	1 TRN5_HUMAN	P25942 myxoma viru
21	203	13.6	289	1 TRN5_MOUSE	P27512 mus musculu
22	202	13.5	269	1 TRN5_BOVIN	O28203 bos taurus
23	194.5	13.0	272	1 TRN4_MOUSE	P47741 mus musculu
24	185	12.4	256	1 TRN9_MOUSE	P20334 mus musculu
25	182	12.2	535	1 TRN8_HUMAN	P28908 homo sapien
26	174	11.7	416	1 TRN9_HUMAN	O07011 homo sapien
27	171.5	11.5	416	1 TR16_CHICK	P18519 gallus gall
28	171	11.5	180	1 TR22_MOUSE	O9er62 mus musculu
29	168	11.3	425	1 TR16_RAT	P07174 rattus norv
30	163	10.9	332	1 TRN6_PIG	O77736 sus scrofa
31	162	10.9	417	1 TR16_MOUSE	O92041 mus musculu
32	158	10.6	427	1 TR16_HUMAN	P08138 homo sapien

34	155.5	10.4	327	1 TRN6_MOUSE	P25446 mus musculu
35	155	10.4	323	1 TRN6_BOVIN	P51867 bos taurus
36	153	10.3	241	1 TR18_HUMAN	O9y505 homo sapien
37	152.5	10.2	430	1 TR1T_MACFA	O9092 macaca fasc
38	151.5	10.2	430	1 TR1T_HUMAN	O96924 mus sapien
39	148.5	10.0	176	1 TR23_MOUSE	O9er63 mus musculu
40	148	9.9	250	1 TRN7_MOUSE	P41272 mus musculu
41	147.5	9.9	5376	1 ZAN_MOUSE	O88799 mus musculu
42	145	9.7	335	1 TRN6_HUMAN	P25445 homo sapien
43	143.5	9.6	471	1 TR1A_BOVIN	O19131 bos taurus
44	142.5	9.6	260	1 TRN7_HUMAN	P26842 homo sapien
45	137.5	9.2	324	1 TRN6_RAT	O63199 rattus norv

## ALIGNMENTS

RESULT 1  
TR6B\_HUMAN STANDARD; PRT; 300 AA.  
ID TR6B\_HUMAN  
AC O95407;  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M6B).  
GN TNFRSF6B OR DCR3 OR TR6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCBI TaxID=9606;  
RX MEDLINE=9067326; PubMed=9872321;  
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A.;  
RA "genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer.";  
RL Nature 396:699-703 (1998).  
RN [2]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.  
RC TISSUE=Prostate;  
RX MEDLINE=99253915; PubMed=10318773;  
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;  
RT "A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";  
RL J. Biol. Chem. 274:13733-13736(1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=20122600; PubMed=10655513;  
RA Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Gallows S.M., Liu Q., Austin C.P., Caskey C.T.;  
RT "Overexpression of M6B/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Matthews L.;  
RN Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF4/LIGHT and TNFSF6/FasL. Protects against apoptosis.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.

CC Detected in adult stomach, spinal cord, lymph node, trachea,  
 CC spleen, colon and lung. Highly expressed in several primary tumors  
 CC from colon, stomach, rectum, esophagus and in SW480 colon  
 CC carcinoma cells.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF104419; AAD03056.1; -  
 CC EMBL; AF134240; AAD29688.1; -  
 CC EMBL; AF217793; AAF35244.1; -  
 CC EMBL; AF217793; AAF33685.1; -  
 CC EMBL; AF217794; AAF33686.1; -  
 CC EMBL; AL121845; AAC03668.1; -  
 CC EMBL; BC017065; AAH17065.1; -  
 CC Genew; HGNC:11921; TNFRSF6B.  
 CC MIM; 603361; -  
 CC HSSP; O14763; 1D0G.  
 CC InterPro; IPR001368; TNFR\_C6.  
 CC Pfam; PF00020; TNFR\_C6; 4.  
 CC ProDom; PD000771; TNFR\_C6; 1.  
 CC SMART; SM00208; TNFR; 3.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 CC PROSITE; PS0050; TNFR\_NGFR\_2; 2.  
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1  
 FT CHAIN 30 300 TUMOR NECROSIS FACTOR RECEPTOR  
 FT  
 FT REPEAT 31 70  
 FT REPEAT 72 113 TNFR-CYS 1.  
 FT REPEAT 115 150 TNFR-CYS 2.  
 FT REPEAT 152 193 TNFR-CYS 3.  
 FT REPEAT 152 193 TNFR-CYS 4.  
 FT DISULFID 49 62 BY SIMILARITY.  
 FT DISULFID 52 70 BY SIMILARITY.  
 FT DISULFID 73 88 BY SIMILARITY.  
 FT DISULFID 91 105 BY SIMILARITY.  
 FT DISULFID 95 113 BY SIMILARITY.  
 FT DISULFID 115 126 BY SIMILARITY.  
 FT DISULFID 132 150 BY SIMILARITY.  
 FT DISULFID 153 168 BY SIMILARITY.  
 FT DISULFID 174 193 BY SIMILARITY.  
 FT CARBOHYD 173 173 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;  
 Query Match 100.0%; Score 1491; DB 1; Length 300;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-110;  
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VAEPTYPWDAETGERLVCAQPPGTFVORPCRRDPTTCGCPPHRYTFWNLYLERCR 60  
 DB 30 VAEPTYPWDAETGERLVCAQPPGTFVORPCRRDPTTCGCPPHRYTFWNLYLERCR 89  
 QY 61 YCNVLGCEEREERARACHATHNRCRKTGFFAHAGFCLHSCPPGAGVIAPGTPSQNTQ 120  
 DB 90 YCNVLGCEEREERARACHATHNRCRKTGFFAHAGFCLHSCPPGAGVIAPGTPSQNTQ 149  
 QY 121 CQCPGPTFGASSSSSSQCPHNRCTALGLALNVPSSSHDTICTCTGTPPLSTRVPGAE 180  
 DB 150 CQCPGPTFGASSSSSSQCPHNRCTALGLALNVPSSSHDTICTCTGTPPLSTRVPGAE 209  
 QY 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGWPTPRAGRAALQKLRRRLTELLGAQD 240  
 DB 210 ECERAVIDFVAFODISIKRLQRLQALEAPEGWPTPRAGRAALQKLRRRLTELLGAQD 269  
 QY 241 GALLVRLQLQALRVARMPGLERSVRERFLPVH 271  
 DB 270 GALLVRLQLQALRVARMPGLERSVRERFLPVH 300

RESULT 2  
 T11B\_HUMAN  
 ID T11B\_HUMAN STANDARD; PRT; 401 AA.  
 AC O00300; O60236; Q9UHP4;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 11B precursor  
 DE (osteoprotegerin) (osteoclastogenesis inhibitory factor).  
 GN TNFRSF11B OR OPB OR OCIF.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=97262071; PubMed=9108485;  
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,  
 RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,  
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,  
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,  
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,  
 RA Suggs S., Boyle W.J.;  
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation  
 RT of bone density.";  
 RL Cell 89:309-319(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung cancer;  
 RX MEDLINE=98151033; PubMed=9492069;  
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,  
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,  
 RA Tsuda E., Morinaga T., Higashio K.;  
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and  
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits  
 RT osteoclastogenesis in vitro.";  
 RL Endocrinology 139:1329-1337(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.  
 RC TISSUE=Placenta;  
 RX MEDLINE=98351569; PubMed=9688283;  
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;  
 RT "Cloning and characterization of the gene encoding human  
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";  
 RL Eur. J. Biochem. 254:685-691(1998).  
 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.  
 RC TISSUE=Eye;  
 RA Strausberg R.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 22-36 AND 378-401.  
 RX MEDLINE=98238445; PubMed=9571159;  
 RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,  
 RA Morinaga T., Tsuda E., Higashio K.;  
 RT "Characterization of monomeric and homodimeric forms of  
 RT osteoclastogenesis inhibitory factor.";  
 RL Biochem. Biophys. Res. Commun. 245:382-387(1998).  
 RN [6]  
 RP SEQUENCE OF 22-393 FROM N.A.  
 RC TISSUE=Placenta;  
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;  
 RT "Cloning and expression of osteoprotegerin from Homo sapiens.";  
 RL Acta Biochim. Biophys. Sin. 31:680-684(1999).  
 RN [7]  
 RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.  
 RX MEDLINE=97312536; PubMed=9168977;  
 RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,  
 RA Morinaga T., Higashio K.;  
 RT "Isolation of a novel cytokine from human fibroblasts that





CC whereas expression decreases at day 11 and increases from day 15  
 CC to 17. On day 15 found in developing bone primordia,  
 CC brachiocephalic artery and ductus arteriosus, left main bronchus,  
 CC abdominal aorta and midgut.  
 CC -1- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by  
 CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 2 DEATH DOMAINS.  
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 CC -----  
 CC EMBL: U94331; AAB5708.1; -.  
 CC EMBL: AB013898; BAA28269.1; -.  
 CC EMBL: AB013903; BAA33388.1; -.  
 CC EMBL: AB013899; BAA33388.1; JOINED.  
 CC EMBL: AB013900; BAA33388.1; JOINED.  
 CC EMBL: AB013901; BAA33388.1; JOINED.  
 CC EMBL: AB013902; BAA33388.1; JOINED.  
 CC HSSP: P25942; 1CDF.  
 CC MGI: 109587; Tnftrf11b.  
 CC InterPro: IPR000488; Death.  
 CC InterPro: IPR001368; TNFR\_c6.  
 CC Pfam: PF00020; TNFR\_c6; 3.  
 CC ProDom: PD000771; TNFR\_c6; 1.  
 CC SMART: SM00005; DEATH; 1.  
 CC SMART: SM00208; TNFR; 4.  
 CC PROSITE: PS50017; DEATH DOMAIN; 1.  
 CC PROSITE: PS00652; TNFR\_NGFR\_2; 2.  
 CC PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 CC Receptor: Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.  
 CC CHAIN 1 21  
 CC 22 401  
 CC 1  
 CC 22 401  
 CC REPEAT 24 62  
 CC REPEAT 65 105  
 CC REPEAT 107 142  
 CC REPEAT 145 185  
 CC DOMAIN 198 269  
 CC DOMAIN 283 365  
 CC SITE 400 400  
 CC DISULFID 41 54  
 CC DISULFID 44 62  
 CC DISULFID 65 80  
 CC DISULFID 83 97  
 CC DISULFID 107 118  
 CC DISULFID 124 142  
 CC DISULFID 145 160  
 CC DISULFID 166 185  
 CC CARBOHYD 98 165  
 CC CARBOHYD 178 178  
 CC CARBOHYD 289 289  
 CC VARIANT 138 138  
 CC VARIANT 161 161  
 CC VARIANT 165 165  
 CC VARIANT 288 288  
 CC VARIANT 296 296  
 CC SEQUENCE 401 AA; 45923 MM; CAA61020B312470 CRC64;  
 Query Match 28.5%; Score 424.5; DB 1; Length 401;  
 Best Local Similarity 39.0%; Pred. No. 1.6e-26;

Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;  
 QY 5 PTYPMDAETGERTLVAQCPPTGFVORPCGRDPTTCGCPPEPHYQFMWYLCRCYCNV 64  
 DB 26 PKLIHNDPERGHOLCDKCAPGYLKHCHTRKTLCPPEPHSYDSMTSDECYCSP 85  
 QY 65 LGEREEBARACHATNHRACRCRTGFPAHAGFLEHASCPEPGAGVIAPTGSONTOCQC 124  
 DB 86 VKELQSVKQECNRTNHRVCECEGRYLEIEFLKHSRCPGSGVQAGTPERNVCKKC 145  
 QY 125 PPGTFSSSSSSQCCPHRCTALGLANVPGSSSDTLCTGTFPLSTRVGAEE--C 162  
 DB 146 PDGFSEETSKAPCIKHNCSTFFGLLIQKGNATHDV--CSGNREATQKGDVTLT 202  
 QY 183 ERAVIDPFAFDISIKRLQRLQAL 207  
 DB 203 EBAFFRAVPTKLIIPMWLSVLDL 227  
 RESULT 5  
 ID TRIB HUMAN STANDARD; PRT; 461 AA.  
 AC P20333; Q16042;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor  
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Ectanecept)  
 DE [contains: Tumor necrosis factor binding protein 2 (TNFRII)].  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins.";  
 RL Science 248:1019-1023 (1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91045991; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335 (1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9629745; PubMed=8661109;  
 RA Bellinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepaelder D., Stallard B.J., Goeddel D.V., Desauvage F.J.;  
 RA Brodeur G.M.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RL Genomics 35:94-100 (1996).  
 RN [4]  
 RP SEQUENCE OF 37-461 FROM N.A.  
 RX MEDLINE=91370690; PubMed=1966549;  
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,  
 RA Brockhaus M., Lesslauer W.;  
 RT "Two human TNF receptors have similar extracellular, but distinct  
 RT intracellular, domain sequences.";  
 RL Cytokine 2:231-237 (1990).  
 RN [5]  
 RP SEQUENCE OF 116-461 FROM N.A. AND PARTIAL SEQUENCE.  
 RX MEDLINE=90349572; PubMed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
 RA Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
 RT and demonstration of a shed form of the receptor.";

Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
[6]  
SEQUENCE OF 27-31.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors."  
RL J. Biol. Chem. 265:1531-1536(1990).  
[7]  
RX SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
RX MEDLINE=91056048; PubMed=2173696;  
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
RA Brockhaus M.;  
RT "Purification and partial amino acid sequence analysis of two  
RT distinct tumor necrosis factor receptors from HL60 cells."  
RL J. Biol. Chem. 265:20131-20138(1990).  
[8]  
RX CHARACTERIZATION.  
RX MEDLINE=93016040; PubMed=1328224;  
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
RA Lipari M.T., Goeddel D.V.;  
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
RT Characterization of ligand binding, internalization, and receptor  
RT phosphorylation."  
RL J. Biol. Chem. 267:21172-21178(1992).  
[9]  
RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
RX TRAF2.  
RX MEDLINE=99221490; PubMed=10206649;  
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
RT "Structural basis for self-association and receptor recognition of  
RT human TRAF2."  
RL Nature 398:533-538(1999).  
CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and  
CC approximately 5-fold lower affinity for homotrimeric  
CC TNFSF1/lymphotoxin-alpha.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -!- PTM: Phosphorylated; mainly on serine residues and with a very low  
CC level on threonine residues.  
CC -!- PTM: A soluble form (tumor necrosis factor binding protein 2) is  
CC produced from the membrane form by proteolytic processing.  
CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and  
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid  
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding  
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to  
CC TNF-alpha and blocks its interactions with receptors.  
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".  
CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
CC WWW="http://www.enbrelinfo.com/".  
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CC -----  
DR EMBL; M32315; AAC59929.1; -  
DR EMBL; U52165; AAC50622.1; -  
DR EMBL; U52156; AAC50622.1; JOINED.  
DR EMBL; U52157; AAC50622.1; JOINED.  
DR EMBL; U52158; AAC50622.1; JOINED.  
DR EMBL; U52159; AAC50622.1; JOINED.  
DR EMBL; U52160; AAC50622.1; JOINED.  
DR EMBL; U52161; AAC50622.1; JOINED.  
DR EMBL; U52162; AAC50622.1; JOINED.  
DR EMBL; U52163; AAC50622.1; JOINED.  
DR EMBL; U52164; AAC50622.1; JOINED.  
DR EMBL; M55994; AAC36755.1; -

DR EMBL; S63368; AAB19824.2; -  
DR EMBL; M35857; AAB63262.1; -  
DR PIR; A35356; A35356.  
DR PIR; A36007; A36007.  
DR PIR; A36475; A36475.  
DR PIR; B35010; B35010.  
DR PIR; A23666; A23666.  
DR PDB; 1CA9; 12-APR-99.  
DR GenSeq; HGNC:11917; TNFRSF1B.  
DR MIM; 191191; -  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR ProDom; PD000771; TNFR\_c6; 1.  
DR SMART; SM00208; TNFR\_4.  
DR PROSITE; PS00852; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00852; TNFR\_NGFR\_2; 4.  
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
KW Phosphorylation; Pharmaceutical; 3D-structure.  
FT SIGNAL 1 22  
FT CHAIN 23 461  
FT CHAIN ?  
FT DOMAIN 23 257  
FT TRANSMEM 258 287  
FT DOMAIN 288 461  
FT REPEAT 39 76  
FT REPEAT 77 118  
FT REPEAT 119 162  
FT REPEAT 163 201  
FT DISULFID 40 53  
FT DISULFID 54 67  
FT DISULFID 57 75  
FT DISULFID 78 93  
FT DISULFID 96 110  
FT DISULFID 100 118  
FT DISULFID 120 126  
FT DISULFID 134 143  
FT DISULFID 137 161  
FT DISULFID 164 179  
FT CARBOHYD 171 171  
FT CARBOHYD 193 193  
FT CONFLICT 141 141  
FT CONFLICT 196 196  
FT CONFLICT 363 363  
SQ SEQUENCE 461 AA; 48291 MW; 603D0AE1CD69ACBF CRC64;  
Query Match 22.8%; Score 340.5; DB 1; Length 461;  
Best Local Similarity 29.7%; Pred. No. 7.6e-20;  
Matches 89; Conservative 43; Mismatches 115; Indels 53; Gaps 11;  
QY 1 VAEPTYPWRDAETGE-----RLVCAQCPPTGVQRPQRDRDPTTCGPPPRH 48  
DB 27 VAFTPYAP-----EPGSTCLREYVDQTAQCCSKSPGQHVCTKTSDTVCDSCEDST 82  
QY 49 YTFQWYLERCRYCNVLCEREEERACHATHNACRCRTGTFAHAG-----FCLHAS 102  
DB 83 YITQLMWVPECLSCGRSCSDQVETQACTREQNRICTRPGWYCALSKQEGCLCAPLRK 142  
QY 103 CPGAGVIAPGTPSOMTQCPPTGTFSSASSSSSQCPHNCNTALGLALNVPSSSHDT 162  
DB 143 CRFGFGVAPGTSTSDVCKPCAPGTFTSTSDICRPHQCNVVA-----IFGNASMDA 198  
QY 163 LCTSTCTGFFLSTRVGAECERCAVIDFVAFQDISIKRLQLQALBAPE-----GNGPTP 217  
DB 199 VCTSTG--PTRSMAPGAVHLPQPV-----STRSQTQTPETPSTAPSTSFLLPMGSP 249  
QY 218 RA-----GRAALQKLRRRLTELLGAODGALLVRLQAL---RVARNP-GLERSVRERFLP 269  
DB 250 PABGSTGDFALPVGLIVGVTL-----GLLIIGVNVNCVIMTVQKKKPLCLQREAKVPHLP 304  
RESULT 6  
TRIB\_MOUSE



```

RX MEDLINE-94225209; PubMed-8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfelds B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor."
RN Science 264:707-710(1994).
RL [4]
RN CHARACTERIZATION.
RP MEDLINE-99223511; PubMed-10207006;
RX Wu M.-Y., Wang P.-Y., Han S.-H., Heieh S.-L.;
RA "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RT death in HeLa cells."
RL J. Biol. Chem. 274:11868-11873(1999).
RL [5]
RN FUNCTION.
RX MEDLINE-20261554; PubMed-10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
RT LIGHT-mediated apoptosis of tumor cells."
RL J. Biol. Chem. 275:14307-14315(2000).
CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC -1- SUBUNIT: Self-associates.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL; L04270; AAA36757.1; --
DR EMBL; BC026262; AAR26262.1; --
DR HSSP; P25942; ICDF.
DR Genew; HGNC:6718; LTBR.
DR MIM; 600979; --
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 31 435
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 3.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM
FT DOMAIN 228 248
FT DOMAIN 249 435
FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
FT SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;
Query Match 20.18; Score 299.5; DB 1; Length 435;
Best Local Similarity 32.04; Pred. No. 1.2e-16;

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Matches 74; Conservative 27; Mismatches 101; Indels 29; Gaps 9;
QY 13 ETGERLVACQPGTGVQPCRDSDPTTCGCPPEPRHYTQFWNYL----ERCYCNVLCGER 69
DB 52 EPOHRIICSCRCPPGTYSKACSRIRDTVCATCAENSYNEHWNLYLTICQLCRPCDPVWG-- 109
QY 70 EEEARACHATHNRACRCRTGFFAHAGFCLE--H---ASCPGGA-GVIAPGTPSQNTQCQ 122
DB 110 LEEIAPCTSKRKTQCKCQGMFC-AAWALECTHCELLSDCPGTEAEKDXEKGNNHCV 168
QY 123 PCPPGTFSSASSSEQCQPHRNCTALGLALNVPGSSSHDTLCTCTGTFPLSTRVPGAEBC 182
DB 169 PCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAAQSDTCKNPLE-PLPPMSGTMLM 227
QY 183 ERAVIDFAVAFQDIS-----IKRLQLLOALEAPEGCGWGTTPRAG 220
DB 228 LAVLLPFLAFLLATVFCIWKSHPSLCRKLGSLLK--RRPQEGNPNVAG 276
RESULT 8
TR21_MOUSE
ID TR21_MOUSE STANDARD; PRT; 655 AA.
AC Q9EPU5; Q91XH9; Q91W77;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor-6 (Death receptor 6).
DE related death receptor-6) (Death receptor 6).
GN TNFRSF21 OR DR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RT "Murine DR6: murine TNFR-related death receptor-6."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE-21571606; PubMed-11714751;
RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal Kinase activity and T cell
RT differentiation in death receptor 6-deficient mice."
RL J. Exp. Med. 194:1441-1448(2001).
CC -1- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC similarity). May activate JNK and be involved in T-cell
CC differentiation.
CC -1- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC May be involved in T-cell differentiation.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC thymus, testis, prostate, ovary, small intestine, colon, brain,
CC lung and kidney, and in fetal brain, liver and lung. Detected at
CC lower levels in adult peripheral blood leukocytes, lung, and in
CC fetal muscle, heart, kidney, small intestine and skin. Detected in
CC T-cells, B-cells and monocytes. In T-cells expression is highest
CC in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

```





```
FT SIGNAL 1 41 POTENTIAL
FT CHAIN 42 655 TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 21.
FT DOMAIN 42 349 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 350 370 POTENTIAL.
FT DOMAIN 371 655 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 415 498 DEATH.
FT REPEAT 50 88 TNFR-CYS 1.
FT REPEAT 90 131 TNFR-CYS 2.
FT REPEAT 133 167 TNFR-CYS 3.
FT REPEAT 170 211 TNFR-CYS 4.
FT DISULFID 67 80 BY SIMILARITY.
FT DISULFID 70 88 BY SIMILARITY.
FT DISULFID 91 106 BY SIMILARITY.
FT DISULFID 109 123 BY SIMILARITY.
FT DISULFID 113 131 BY SIMILARITY.
FT DISULFID 133 144 BY SIMILARITY.
FT DISULFID 150 168 BY SIMILARITY.
FT DISULFID 171 186 BY SIMILARITY.
FT DISULFID 192 211 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 19.2%; Score 287; DB 1; Length 655;
Best Local Similarity 34.3%; Pred. No. 1.8e-15;
Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;

QY 6 TYPRDRAETGERLVCAQCPGTFVQRCRRDSDPTGCPPRHYTQFWNYLCRYCNVL 65
Db 53 TYRHVDRATGOVLTCDCPCAGTVVSEHTCTSLRVCSGCPVGTFRHENGIEKCHDCSQP 112
QY 66 CGREEREARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAFGTSPQNTQCP 125
Db 113 CPWPMIEKLPKCAALTDRECTCPPGFMOSNATCAPHTVCPGVGVRKKGTTEDVRCKQCA 172
QY 126 PGTFSSASSSEOCOPHRNCTALGLALNVPGSSSHDTLCTCTGFFPLST 174
Db 173 RGTFSDVPSSVMKCKATYDCLSQLNVIKPGTKETDNCVGLTSPFSST 221

RESULT 10
TNR3 MOUSE
ID TNR3 MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (lymphotoxin-beta receptor).
GN LTRB OR TNFRSF3 OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RL J. Immunol. 155:5280-5288 (1995).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
```

```
RT RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs
CC (By similarity)
CC -!- SUBUNIT: Self-associates (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U29173; AAA68964.1; -.
CC EMBL; U38423; AAB00846.1; -.
CC EMBL; U30798; AAA81334.1; -.
CC HSSP; O14763; IDOG.
CC MGD; MGI:104875; Ltbr.
CC InterPro: IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 3.
CC ProDom; PD000771; TNFR_C6; 1.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00500; TNFR_NGFR_2; 3.
CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 415 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 224 244 SUPERFAMILY MEMBER 3.
FT DOMAIN 245 415 POTENTIAL.
FT REPEAT 42 81 CYTOPLASMIC (POTENTIAL).
FT REPEAT 82 124 TNFR-CYS 1.
FT REPEAT 125 170 TNFR-CYS 2.
FT REPEAT 171 213 TNFR-CYS 3.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 142 169 BY SIMILARITY.
FT DISULFID 172 187 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 17.8%; Score 265.5; DB 1; Length 415;
Best Local Similarity 30.9%; Pred. No. 5.6e-14;
Matches 72; Conservative 24; Mismatches 88; Indels 49; Gaps 10;

QY 20 CAQCPGTFVQRCRRDSDPTGCPPRHYTQFWNYL---ERCRCYNVLCGEREEARAC 76
Db 59 CSRCPPGFEFVAVCSQDVTCKTCHNSYNHWNHLSQLCRCPCDIVLG--FEVAPC 116
QY 77 HATHNACRCRTGFFAHAGFCLE---EHASCPGAGVIA-PGTPSQNT-----QCQP 123
Db 117 TSDRKAECRCQPM-----SCVLDNECVHCEBERLVLCQGTAEVTDIMTDVNCVP 171
QY 124 CPPTGTSASSSSEOCOPHRNCTALGLALNVPGSSSHDILCTCTGFFPLSTRVGAEECE 183
Db 172 CKPGHFONTSSPRARCOPHTRCIEQGLVEAAPGTYSYDICK-----NPPEFGAMLL 224
QY 184 RAVIDFVAF-----QDISIKRLQRLQLALEAPEGMG-----PTPRA 219
```

Db 225 ALLSLVLFLLFTTVALACAMRHPSLCKRLGLTK--RHPEGEESPCCAPRA 275

RESULT 11

CRMB\_VARV STANDARD; PRT; 349 AA.

ID P34015; Q89098; Q85407; Q89118;

AC 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Soluble TNF receptor II precursor (cytokine response modifying protein B).

GN CRMB OR G2R OR G4R.

OS Variola virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.

OX NCBI\_TaxID=10255;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=India-1967 / Isolate Ind;

RA MEDLINE=93202281; PubMed=8384129;

RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;

RT "Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.";

RL FEBS Lett. 319:80-83(1993).

RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN=Bangladesh-1975;

RA MEDLINE=94088747; PubMed=8264798;

RA Masung R.F., Eposito J.C., Liu L., Qi J., Uteback T.R., Knight J.C., Audin L., Yuran T.E., Parsons J.M., Loparev V.N., Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J., Venter C.J.;

RT "Potential virulence determinants in terminal regions of variola smallpox virus genome.";

RL Nature 366:748-751(1993).

RN (3)

RP SEQUENCE FROM N.A.

RC STRAIN=Garcia-1966, and Somalia-1977;

RA Masung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M., Totmenin A.V., Shchelkunov S.N., Eposito J.C.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

RN (4)

RP SEQUENCE FROM N.A.

RC STRAIN=Garcia-1966;

RA MEDLINE=20107289; PubMed=10639322;

RA Shchelkunov S.N., Totmenin A.V., Loparev V.N., Saifonov P.F., Gutarov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Masung R.F., Eposito J.C.;

RT "Alaetrim smallpox variola minor virus genome DNA sequences.";

RL Virology 266:361-386(2000).

RN (5)

RP SEQUENCE FROM N.A.

RC STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;

RA Loparev V.N., Parsons J.M., Eposito J.C.;

RT "DNA sequence analysis as a criterion for allocation of the orthopoxviruses to a particular species.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes (By similarity).

-1- SUBCELLULAR LOCATION: Secreted (By similarity).

-1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.

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CC EMBL; X69198; CAA49137.1; -

DR EMBL; X67117; CAA47540.1; -

DR EMBL; L22579; AAA60933.1; -

DR EMBL; U18339; AAA69407.1; -

DR EMBL; U18341; AAA69467.1; -

DR EMBL; Y16780; CAB54798.1; -

DR EMBL; U88146; AAB94371.1; -

DR EMBL; U88148; AAB94373.1; -

DR EMBL; U88149; AAB94374.1; -

DR EMBL; U88152; AAB94377.1; -

DR PIR; D36858; D36858.

DR PIR; S35987; S35987.

DR PIR; S46888; S46888.

DR HSSP; O14763; 1D0G.

DR InterPro: IPR001368; TNFR\_c6.

DR Pfam: PF00020; TNFR\_c6; 2\_

KM Receptor; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 22

FT CHAIN 23 349

FT REPEAT 31 66

FT REPEAT 67 108

FT DISULFID 32 43

FT DISULFID 44 57

FT DISULFID 47 65

FT DISULFID 68 83

FT DISULFID 86 100

FT DISULFID 90 108

FT CARBOHYD 101 101

FT CARBOHYD 173 173

FT CARBOHYD 189 189

FT CARBOHYD 215 215

FT CARBOHYD 248 248

FT VARIANT 17 17

FT VARIANT 160 160

FT VARIANT 165 165

FT VARIANT 182 182

FT VARIANT 274 274

FT VARIANT 335 335

FT VARIANT 339 339

FT SEQUENCE 349 AA; 38189 MW; D45D40B5C6E780EF CRC64;

SQ

Query Match 17.4%; Score 260; DB 1; Length 349;

Best Local Similarity 32.2%; Pred. No. 1,3e-13; Mismatches 90; Indels 8; Gaps 3;

Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWDAE-TGERLYCAOCPPTGVQPCRDSPPTCGPCPPRHAYTOFWNNYLERGRYCN 63

Db PNRKCDTEYKRNRLCLSPPTVARSRLCDSKTNOCPTCGSGTTSRNHLPALCLSCN 87

QY 64 VLGERBEERACHATHNRACRCRTGPF-----AHAGFLEHASCPGAGVAPGTPSQ 117

Db GRGNSNQVETRSNTTHNRICCSPGYCYLKGSSCKACVSGTKGIGYGV-SGHTSVG 146

QY 118 NTCOCPCPTGFASSSSBQCPHRNCTALGLALNVPSSSHDTLCTSGTSPFLSTRVP 177

Db DVICSPCGRTYSHVTSADKCEPVNNTFNVIDETILYPVNDISCTRTTTGTSLSIL 206

QY 178 GAE 180

Db 207 TSE 209

RESULT 12

CRMB\_CAMPS STANDARD; PRT; 349 AA.

AC Q8UYA7;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Soluble TNF receptor II precursor (cytokine response modifying protein  
DE B).  
GN (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP20SR OR CMLV210).  
OS Camelpox virus (strain CMS), and  
OS Camelpox virus (strain M-96).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=203172, 203173;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CMS;  
RX PubMed=11907336;  
RA Gubser C., Smith G.L.;  
RT "The sequence of camelpox virus shows it is most closely related to  
RT variola virus, the cause of smallpox.";  
RN J. Gen. Virol. 83:855-872(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=M-96;  
RA Afonso C.L., Tulman E.R., Lu Z., Zaitsev V.L.,  
RA Kerembekova U.Z., Sandyaev N.T., Kutish G.F., Rock D.L.;  
RT "The genome of camelpox virus.";  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to  
CC the modification of TNF-mediated antiviral processes (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
CC  
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CC  
CC EMBL; AY009089; AAG37456.1; -  
CC EMBL; AY009089; AAG37718.1; -  
CC EMBL; AF438165; AAL73920.1; -  
CC EMBL; AF438165; AAL73917.1; -  
CC InterPro: IPR001368; TNFR\_C6.  
CC Pfam; PF00020; TNFR\_C6; 2.  
CC SMART; SM00208; TNFR\_3.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
CC PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
KW Receptor; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 349 SOLUBLE TNF RECEPTOR II.  
FT REPEAT 31 65 TNFR-CYS 1.  
FT REPEAT 67 108 TNFR-CYS 2.  
FT DISULFID 32 43 BY SIMILARITY.  
FT DISULFID 44 57 BY SIMILARITY.  
FT DISULFID 47 65 BY SIMILARITY.  
FT DISULFID 68 83 BY SIMILARITY.  
FT DISULFID 86 100 BY SIMILARITY.  
FT DISULFID 90 108 BY SIMILARITY.  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 349 AA; 38064 MW; EA412AF991E087F3 CRC64;  
Query Match 17.3%; Score 257.5; DB 1; Length 349;  
Best Local Similarity 32.0%; Pred. No. 2e-13;  
Matches 54; Conservative 28; Mismatches 80; Indels 7; Gaps 2;  
QY 18 LVCAQCPGGTGVORPCRRDSTTCGPPRRHYTFQFMYNLCRCYCNVLCGEREEARACH 77  
DB 42 LCLLSCPPGGYASRLCDKNTKTCGSGTFTSRNNHLPACLSCNCRCDNQVETRSCN 101

QY 78 ATHNRACRGTGFF-----AHAGFCLEHASCPGAGVIAPGTPSONTOCQCPGCTFSA 131  
DB 102 TTHNRICECPGYCYLKSGCKACVSKTGIGYGV-SGHTSAGDVICSPGCLGTYSR 160  
QY 132 SSSSSQCCOPHRNCTALGLALNVPGSSSDTLCTCTGFPPLSTRVPGAEE 180  
DB 161 TVSSADKCEPVSNTFNVDINLPVNDTCTRTTTTGISESISTSE 209  
RESULT 13  
ID\_CRM COMPX STANDARD; PRT; 351 AA.  
AC Q73559;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Soluble TNF receptor II precursor (cytokine response modifying protein  
DE B).  
GN (CRMB1 OR D2L) AND (CRMB2 OR H4R).  
OS Cowpox virus (CPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
OX NCBI\_TaxID=10243;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GRI-90 / Grishak;  
RX MEDLINE=98229462; PubMed=9568042;  
RA Shchelkunov S.N., Safonov V.V., Totmenin A.V., Petrov N.A.,  
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;  
RT "The genomic sequence analysis of the left and right species-specific  
RT terminal region of a cowpox virus strain reveals unique sequences and  
RT a cluster of intact ORFs for immunomodulatory and host range  
RT proteins.";  
RL Virology 243:432-460(1998).  
RN [2]  
RP FUNCTION.  
RC STRAIN=Brighton red;  
RX PubMed=8091665;  
RA Hu F.Q., Smith C.A., Pickup D.J.;  
RT "Cowpox virus contains two copies of an early gene encoding a soluble  
RL secreted form of the type II TNF receptor.";  
RL Virology 204:343-356(1994).  
CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to  
CC the modification of TNF-mediated antiviral processes.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
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CC  
CC EMBL; Y11842; CAA72578.1; -  
CC EMBL; Y15035; CAA75306.1; -  
CC HSSP; O14763; IDOG.  
DR InterPro: IPR001368; TNFR\_C6.  
DR Pfam; PF00020; TNFR\_C6; 2.  
DR SMART; SM00208; TNFR\_2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
KW Receptor; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 351 SOLUBLE TNF RECEPTOR II.  
FT REPEAT 31 67 TNFR-CYS 1.  
FT REPEAT 69 110 TNFR-CYS 2.  
FT DISULFID 32 43 BY SIMILARITY.  
FT DISULFID 44 57 BY SIMILARITY.  
FT DISULFID 47 67 BY SIMILARITY.  
FT DISULFID 70 85 BY SIMILARITY.

FT DISULFID 86 102 BY SIMILARITY.  
 FT DISULFID 92 110 BY SIMILARITY.  
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 351 AA; 38253 MW; 57CAE73EFAE5D7C7 CRC64;  
 Query Match 17.1%; Score 254.5; DB 1; Length 351;  
 Best Local Similarity 32.2%; Pred. No. 3.4e-13;  
 Matches 55; Conservative 29; Mismatches 78; Indels 9; Gaps 3;  
 QY 18 LVAQCPGPGFVVRPC--RRDSPTTGCPGPPHRYTQPMYVLEHCRVCNVLGGEREERARA 75  
 DB 42 LCLSCPPGTVYARLDCSKTNTTQCTPCGSGTFSNNHLPACTLSCNGRCDNQEYETRS 101  
 QY 76 CHATHRACRCRTGFF-----AHAGFLEHASCPPGAGVIAPGTPSQNTQCCPCCPGTF 129  
 DB 102 CHTTHRICCAAGYCYLKGSSGCCACVSGTCGIGYV-SGHTSTGADVCSPPCLGTY 160  
 QY 130 SASSSSSEOCQPHRNCTALGLALNVPSSSHDYLCTSGTGPPLSTVPGAE 180  
 DB 161 SHTVSSADNCEPVPSTNPNYIDVEINLYPNVDISCTRTTGTGSEISITSE 211  
 RESULT 14  
 ID TRI4 HUMAN STANDARD; PRT; 283 AA.  
 AC 092356; Q9UM65; Q96J31; O8WKX1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 14 precursor  
 DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)  
 DE (TR2).  
 GN TNFRSF14 OR HVEM OR HVEA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cervical adenocarcinoma;  
 RX MEDLINE=97053782; PubMed=8898196;  
 RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;  
 RT "Herpes simplex virus-1 entry into cells mediated by a novel member of  
 the TNF/NGF receptor family.";  
 RL Cell 87:427-436(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97306336; PubMed=9162061;  
 RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,  
 Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,  
 Porter J.G., Itruen A., Young P.R.;  
 RT "A newly identified member of the tumor necrosis factor receptor  
 superfamily with a wide tissue distribution and involvement in  
 lymphocyte activation.";  
 RL J. Biol. Chem. 272:14272-14276(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Wan T., Gao X.;  
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.  
 RX MEDLINE=21629477; PubMed=11756979;  
 RA Struyf F., Posavad C.M., Keyaerts E., Van Ranst M., Corey L.,  
 Spear P.G.;  
 RT "Search for polymorphisms in the genes for herpesvirus entry mediator,  
 Nectin-1, and Nectin-2 in immune seronegative individuals.";  
 RL J. Infect. Dis. 185:36-44(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.  
 RX MEDLINE=21403268; PubMed=11511370;  
 RA Carfi A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,  
 RA Eisenberg R.J., Wiley D.C.;  
 RT "Herpes simplex virus glycoprotein D bound to the human receptor  
 Hvea.";  
 RL Mol. Cell 8:169-179(2001).  
 CC -I- FUNCTION: Receptor for TNFRSF14/LIGHT and homotrimeric  
 TNFRSF14/lymphotoxin-alpha. Involved in lymphocyte activation. Plays  
 an important role in HSV pathogenesis because it enhanced the  
 entry of several wildtype HSV strains of both serotypes into CHO  
 cells, and mediated HSV entry into activated human T cells.  
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
 CC -I- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION  
 IN LUNG, SPLEEN, AND THYMUS.  
 CC -I- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL, U70321; AAB58354.1; -.  
 DR EMBL, U81232; AAD00505.1; -.  
 DR EMBL, AF153978; AAF75588.1; -.  
 DR EMBL, AF373877; AAL4771.1; -.  
 DR EMBL, AF373878; AAL47718.1; -.  
 DR EMBL, BC002794; AA02794.1; -.  
 DR PDB, 1JMA: 26-SEP-01.  
 DR Genew; HGNC:11912; TNFRSF14.  
 DR MIM; 602746; -.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR Prodom; PD000771; TNFR\_c6; 1.  
 DR SMART; SM00208; TNFR\_3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;  
 KW 3D-structure.  
 FT SIGNAL 1 38  
 FT CHAIN 39 283  
 FT DOMAIN 39 202  
 FT TRANSMEM 203 223  
 FT DOMAIN 224 283  
 FT REPEAT 42 75  
 FT REPEAT 78 119  
 FT REPEAT 121 162  
 FT DISULFID 42 53  
 FT DISULFID 54 67  
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 FT DISULFID 96 111  
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 FT DISULFID 127 135  
 FT CARBOHYD 110 110  
 FT CARBOHYD 173 173  
 FT VARIANT 17 17  
 FT VARIANT 241 241  
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 FT SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;  
 SQ  
 Query Match 16.4%; Score 244; DB 1; Length 283;  
 Best Local Similarity 37.3%; Pred. No. 1.8e-12;  
 Matches 56; Conservative 14; Mismatches 68; Indels 12; Gaps 4;



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 6, 2003, 11:26:15 ; Search time 51 Seconds  
(without alignments)  
1629.596 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491  
Sequence: 1 VAEPTYPWRDAETGERLVC.....RVAMPGLERSVEREFLPVH 271

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/prodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1491	100.0	1164	2	US-08-794-796-1
2	1491	100.0	1347	4	US-09-286-529-18
3	1339	89.8	1859	4	US-09-286-529-19
4	841	56.4	459	4	US-09-286-529-7
5	440.5	29.5	1355	3	US-08-974-022-5
6	440.5	29.5	1355	4	US-08-795-445A-5
7	440.5	29.5	1355	4	US-08-795-447A-5
8	440.5	29.5	1355	4	US-08-974-186-5
9	440.5	29.5	1355	4	US-08-795-446B-5
10	440.5	29.5	1355	4	US-08-706-945D-127
11	433	29.0	525	3	US-08-997-918-47
12	425.5	28.5	2432	3	US-08-974-022-1

13	425.5	28.5	2432	4	US-08-795-445A-1	Sequence 1, Appl1
14	425.5	28.5	2432	4	US-08-795-447A-1	Sequence 1, Appl1
15	425.5	28.5	2432	4	US-08-974-186-1	Sequence 1, Appl1
16	425.5	28.5	2432	4	US-08-795-446B-1	Sequence 1, Appl1
17	425.5	28.5	2432	4	US-08-706-945D-123	Sequence 123, App
18	424.5	28.5	1324	3	US-08-974-022-3	Sequence 3, Appl1
19	424.5	28.5	1324	4	US-08-795-445A-3	Sequence 3, Appl1
20	424.5	28.5	1324	4	US-08-795-447A-3	Sequence 3, Appl1
21	424.5	28.5	1324	4	US-08-974-186-3	Sequence 3, Appl1
22	424.5	28.5	1324	4	US-08-795-446B-3	Sequence 3, Appl1
23	424.5	28.5	1324	4	US-08-706-945D-125	Sequence 125, App
24	344.5	23.1	1557	1	US-08-585-229-3	Sequence 3, Appl1
25	342	22.9	1641	1	US-08-385-229-1	Sequence 1, Appl1
26	342	22.9	1641	2	US-08-650-000-1	Sequence 1, Appl1
27	342	22.9	1641	6	5395760-1	Patent No. 5395760
28	342	22.9	2224	4	US-08-477-347-2	Sequence 2, Appl1
29	342	22.9	2224	4	US-08-476-862-1	Sequence 1, Appl1
30	342	22.9	3683	4	US-09-844-634-3	Sequence 1, Appl1
31	340	22.8	705	4	US-09-326-394-3	Sequence 3, Appl1
32	338	22.7	705	4	US-09-580-235-1	Sequence 1, Appl1
33	338	22.7	705	4	US-09-580-235-7	Sequence 7, Appl1
34	338	22.7	705	4	US-09-580-181-1	Sequence 7, Appl1
35	338	22.7	705	4	US-09-580-181-7	Sequence 7, Appl1
36	338	22.7	705	4	US-09-102-530-1	Sequence 1, Appl1
37	338	22.7	705	4	US-09-102-530-7	Sequence 7, Appl1
38	337	22.6	705	4	US-09-580-235-3	Sequence 3, Appl1
39	337	22.6	705	4	US-09-580-235-5	Sequence 5, Appl1
40	337	22.6	705	4	US-09-580-181-3	Sequence 3, Appl1
41	337	22.6	705	4	US-09-580-181-5	Sequence 5, Appl1
42	337	22.6	705	4	US-09-102-530-3	Sequence 3, Appl1
43	337	22.6	705	4	US-09-102-530-5	Sequence 5, Appl1
44	332.5	22.3	3796	2	US-08-762-308-11	Sequence 11, Appl1
45	332.5	22.3	3796	4	US-09-844-634-10	Sequence 10, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-794-796-1  
Sequence 1, Application US/08794796  
Patent No. 5885800  
GENERAL INFORMATION:  
APPLICANT: Emery, John  
APPLICANT: Tan, KB  
APPLICANT: Truneh, Alem  
TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794, 796  
FILING DATE: 04-FEB-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Han, William T  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: GH50000  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5219  
TELEFAX: 610-270-4026  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1164 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-794-796-1

Alignment Scores:  
Pred. No.: 1,25e-109 Length: 1164  
Score: 1491.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-09-936-024-1 (1-271) x US-08-794-796-1 (1-1164)

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QY 1 ValAlaGluThrProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
DB 198 GTGGCAGAAACACCCACCTACCTCGCGGGACGACAGACAGGGGAGCGGTGGTGTGC 257
QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
DB 258 GCCCAGTGGCCCCCAGGCACCTTTGTGCAGCGCGCGTGGCGCGACAGACGCCACGACG 317
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
DB 318 TGTGGCCCCGTGTCCACCGCGCCACTACACGAGTTCTTGGAACTACCTGGAGCGCTCCGC 377
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
DB 378 TACTGCAACGTCTCTCGGGGAGCGTGAGGAGGAGGACCGGCTTGGCCACGCCACCCAC 437
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
DB 438 AACCGTGCTCGCGCTCGCCACCGCGCTTCTCGCGACCGCTTCTGCTTGGAGCAC 497
QY 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
DB 498 GCATCGTGTCCACTGGTGGCGCGGTGATTGGCCCGGGCACCCCCAGCAGAACACGACG 557
QY 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
DB 558 TGCACGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCACG 617
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
DB 618 CCCCACCGCAACTGCACGGCCCTGGGCGCTGGCCCTCAATGTGCAGGCTCTTCTCCCAT 677
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
DB 678 GACACCTGTGCACCGCTGCATGGCTTCCCTCCCTCAGCACCAGGTACAGAGGCTGAG 737
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200
DB 738 GAGTGTGAGCGTGCCTCATCGACTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 797
QY 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220
DB 798 CAGCGGCTGTGCAGGCCCTCGAGGCCCGCGAGGGCTGGGGTCCGACACCAAGGGGGGC 857
QY 221 ArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
DB 858 CGCGGGCTTGCAGCTGAAGCTGCGTCGCGCGCTCACGAGGCTCTCGGGGGCGCAGGAC 917
QY 241 GlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
DB 918 GGGGCGCTGCTGGTGGCTGTGTGACGGCGCTGCGCGTGGCCAGGATGCCCGGCTGGAG 977
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QY 261 ArgSerValArgGluArgPheLeuProValHis 271
DB 978 CGGAGCGTCCGTGAGCGCTTCTCCTCGTCAC 1010
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## RESULT 2

US-09-286-529-18  
Sequence 18, Application US/09286529  
Patent No. 6297367  
GENERAL INFORMATION:  
APPLICANT: Catherine Tribouley  
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
FILE REFERENCE: 1408.003/200130.439C1  
CURRENT APPLICATION NUMBER: US/09/286,529  
CURRENT FILING DATE: 1999-04-05  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 18  
LENGTH: 1347  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-286-529-18

Alignment Scores:  
Pred. No.: 1,53e-109 Length: 1347  
Score: 1491.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-936-024-1 (1-271) x US-09-286-529-18 (1-1347)

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QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
DB 465 GCCCAGTGGCCCCCAGGCACCTTTGTGCAGCGCGCTGGCGCGACAGACGCCACGACG 524
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
DB 525 TGTGGCGCGTGTCCACCGCGCCACTACACGCACTTCTGGAACCTACTGGAGCGCTGCCGC 584
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
DB 585 TACTGCAACGTCTCTCGGGGAGCGTGAGGAGGAGGACCGGCTTGCACGCCACCCAC 644
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
DB 645 AACCGTGCTGCGCTGCGCACCGCTTCTTCGCGCACGCTTCTGCTTGGAGCAC 704
QY 101 AlaSerCysProGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
DB 705 GCATCGTGTCCACTGGTGGCGCGTGATTGCCCGGGACCCCCCAGCCAGAACACGACG 764
QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGln 140
DB 765 TGCACAGCGTGGCCCCCAGGCACCTTCTCAGCCACGAGCTCCAGCTCAGAGCAGTGCACG 824
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
DB 825 CCCCACCGCAACTGCACGGCCCTGGGCGCTTCAATGTGCCAGGCTCTTCTCTCCCAT 884
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
DB 885 GACACCTGTGCACCGCTGCATGGCTTCCCTCCAGCACCAGGCTACCCAGGAGCTGAG 944
QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
DB 945 GAGTGTGAGCGTGGCGCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 1004
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QY 201 GlnArgLeuLeuGlnAlaLeuGlnAlaProGluGlyTyrGlyProThrProArgAlaGly 220  
Db 1005 CAGGGGCTGTGAGGCGCTCGAGGCGCCGAGAGGGCTGGGGTCCGACACCAAGGGCGGGC 1064  
QY 221 ArgAlaAlaLeuGlnLeuLeuLeuArgArgArgLeuThrGluLeuGlyValGlnAsp 240  
Db 1065 CGCGCGGCTTGGCAGCTGAGCTGCTGGCGGCTCAGGAGCTTCGGGGGCGCAGAGC 1124  
QY 241 G1yAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260  
Db 1125 GGGGCGCTGCTGGTCCGGCTGCTGAGGCGCTGCGGCTGGCCAGGATGCCGGGCTGAG 1184  
QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
Db 1185 CGAGCGTCCGTGAGCGCTTCTCTCTGTGCAC 1217  
RESULT 3  
US-09-286-529-19  
; Sequence 19, Application US/09286529  
; Patent No. 6297367  
; GENERAL INFORMATION:  
; APPLICANT: Catherine Tribouley  
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
; FILE REFERENCE: 1408,003/200130,439C1  
; CURRENT FILING DATE: 1999-04-05  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PaateSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 1859  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-286-529-19  
Alignment Scores:  
Pred. No.: 2,69e-97 Length: 1859  
Score: 1339.00 Matches: 271  
Percent Similarity: 51.72% Conservative: 0  
Best Local Similarity: 51.72% Mismatches: 0  
Query Match: 89.81% Indels: 253  
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US-09-936-024-1 (1-271) x US-09-286-529-19 (1-1859)  
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QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgSerProThrThr 40  
Db 225 GCCCAGTCCCGCCAGGACCTTGTGTGAGGCGCGCTGCCCGCAGACAGCCCAACAGC 284  
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTyrPasnTyrLeuGluArgCysArg 60  
Db 285 TGTGGCCCGTGTCCACCGCGCACCTACGAGATTCTGAATCACTGAGACGCTGCCGC 344  
QY 61 TyrCysAsnValLeuGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80  
Db 345 TACGCAACGCTCTGTGGGAGGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 404  
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100  
Db 405 AACCTGCTCCGCTGCGTCCGACCGGCTTCTTCGCGACGCTGTTCTGTGGAGAC 464  
QY 101 AlaserCysProProGlyValGlyValIleAlaProGlyTyrProSerGlnAsnThrGln 120  
Db 465 GCATGCTTCCACCTGCGCGGCGGTGATTGCCCGGAGCAACCCAGCAACAAACAGCAG 524  
QY 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSer 140  
Db 525 TGCCAGCCGTCGCCCGGAGGACCTTCTCAGCAGCACTCCAGCTCAGACAGGAGGAGCAG 584  
QY 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160

Db 585 CCCCACCGCAACTGACAGGCGCTGGGCTTGGCCCTCATGTGCGAGGCTTCTCCCAT 644  
QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerHisArgValPro----- 177  
Db 645 GACACCTGTGACACCACTGACTGCTTCCCTCCAGCACAGGATGACAGGATGAGCA 704  
QY 177 ----- 177  
Db 705 GAGGCTGAGGGGGGACACACTGACAGGCCAGGCCACTTGTGCCCTCACTCCTGCCCT 764  
QY 177 ----- 177  
Db 765 GCAGTCATCTAGCTGAGGATGACGCTGCTGGGAGGGGACACAGTGATTTG 824  
QY 177 ----- 177  
Db 825 AGGGTGAGGGGTCCTCCACTAGATCCCAACCAAGTCTGCTTCCAGGGGTGGCTGAG 884  
QY 177 ----- 177  
Db 885 AATTGATCTGAGCAGGAGGACAGCTCCCTGGAGAGCTCTGGAAAGTGGGACGAA 944  
QY 177 ----- 177  
Db 945 TCTCTAATGCCCCGAGGGAGAGGTGGCTGCTCTCTGACAGGGGAAACGAGGCTG 1004  
QY 177 ----- 177  
Db 1005 ATGGTAATCTCTTAATCTGCTGAGAGAGGTGGCTGCTCTCTGACATGGGAAAC 1064  
QY 177 ----- 177  
Db 1065 GAGGCCAATGTTAACCACTGTTGAGAAATGACAGGGGAGATGACCCCTTAATCA 1124  
QY 177 ----- 177  
Db 1125 GTGAGTCCGGTCCATCTGAGGATCCCAACTCGCCCTTCGATGCGGAGGCCCA 1184  
QY 177 ----- 177  
Db 1185 GCCCTGCTGGGCCCCCTTCTCTTTCAGCAAGGTCCGAGTCCGCTCTGCCCCC 1244  
QY 177 ----- 177  
Db 1245 TAGGCTTTGCTCAGCTCTCTGACGAGGCTCTGCCCCCTTCCAGTCCCATCGTT 1304  
QY 177 ----- 177  
Db 1305 GCACTGCCCTCCAGCAGGCTCAGTCAAGGATTTCTCTCTCTGCAACCCCCC 1364  
QY 177 ----- 177  
Db 1365 AGTGGGCGCCAGAAAGAGGATCTTGGCAGCCCCCGCAGTGTGTGTGTAATGAT 1424  
QY 178 -----G1yAlaGluGluCysGluArgAlaValIleAs 168  
Db 1425 CGGACCGCTGCTCCCAACCCACTGCAAGGAGCTGAGAGGTGAGGCTGCTCCATCGA 1484  
QY 188 PheValAlaPheGlnAspIleSerIleLeuArgLeuGlnArgLeuGlnAlaLeuGln 208  
Db 1485 CTTTGTGGCTTCCAGGACATCTCCATCAAGAGGCTGACAGGCTGTCAGGCGCTCGA 1544  
QY 208 uAlaProGluGlyTyrGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuGly 228  
Db 1545 GGGCCCGAGGGGCTGGGGTCCGACACCAAGGGGCGGCGGCTTTCAGCTGAAGCT 1604  
QY 228 uArgArgArgLeuThrGluLeuGlnValGlnAspGlyValLeuLeuValArgLeu 248  
Db 1605 GCGTGGCGGCTCAGGAGCTCTGGGGGCGCAGAGGGGCGCTGTGTGGTGGCTGCT 1664  
QY 248 uGlnAlaLeuArgValAlaArgMetProGlyLeuGluArgSerValArgGluArgPhe 268

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Db 1665 GCAGCGCTGGCGTGGCAGGATGCCGGCTGGAGCGGCGCTCGTGAGCGCTTCCT 1724
Qy 268 uProValHis 271
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Db 1725 CCCTGTGCAC 1734

RESULT 4
US-09-286-529-7
; Sequence 7, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Triboulev
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-286-529-7

Alignment Scores:
Pred. No.: 1,21e-58 Length: 459
Score: 841.00 Matches: 153
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 56.41% Indels: 0
DB: 4 Gaps: 0

US-09-936-024-1 (1-271) x US-09-286-529-7 (1-459)
Qy 56 LeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAla 75
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Db 1 CTGGAGCGCTGGCGTACTGCAACGTCCTCTGCGGGAGCGTGAGGAGGCGACGGGCT 60
|||
Qy 76 CysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGly 95
|||
Db 61 TGCCAGCCACCCACACACCGTGGCGCTGCGCGTGGCGACCGCTTCTTGGCGCACGGTGGT 120
|||
Qy 96 PheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrPro 115
|||
Db 121 TTCTGCTTGGAGCAGCATCGTGTCCACCTGGTGGCGCGTGGTGGCGCGGCGACCCCC 180
|||
Qy 116 SerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSer 135
|||
Db 181 AGCCAGNACAGCAGTGCAGCGTGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
|||
Qy 136 SerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPro 155
|||
Db 241 TCAGAGCAGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
|||
Qy 156 GlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArg 175
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Db 301 GGCTCTTCTCTCCCATCACACCTGTGCACCGTGGCTGGCTGGCTGGCTGGCTGGCTGG 360
|||
Qy 176 ValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIle 195
|||
Db 361 GTACACGAGAGCTGAGGAGTGTGAGCGTGGCGCTCATCGACTTTGTGGCTTTCAGGACATC 420
|||
Qy 196 SerIleLysArgLeuGlnArgLeuLeuGlnAlaLeuGlu 208
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Db 421 TCCATCAAGAGGCTGCAGCGGCTGCTGCAGCGCGCTGCAGCGCGCTGCAG 459
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RESULT 5
US-08-974-022-5
; Sequence 5, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
```

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; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1355 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 94...1296
US-08-974-022-5

Alignment Scores:
Pred. No.: 3,05e-26 Length: 1355
Score: 440.50 Matches: 77
Percent Similarity: 57.75% Conservative: 31
Best Local Similarity: 41.8% Mismatches: 74
Query Match: 29.54% Indels: 5
DB: 3 Gaps: 2

US-09-936-024-1 (1-271) x US-08-974-022-5 (1-1355)
Qy 5 ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
|||
Db 169 CCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTGTGTGACAAATGTCT 228
|||
Qy 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44
|||
Db 229 CTGTGTACTACTATAAACACACTGTACAGCAAGTGGAGAACCGCTGTGCCCGCTTGC 288
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Qy 45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64
|||
Db 289 CTGTACCCTACTACACAGACAGCTGGCACCAGTGGCAGTGTCTATCTACTGCAGCCCC 348
|||
Qy 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
|||
Db 349 GTGTCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCATCGCACCCACCAACCGCGTGC 408
|||
Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104
|||
Db 409 GAATCAAGAGGCGGTCTTGTGAGTAGAGTCTGTCTTGAACATAGGAGTCCCT 468
|||
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
|||
Db 469 CTGTGATTGGAGTGTGCAAGCTGGNAACCCAGAGCGAAATACAGTTTGCAAAAGATGT 528
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Qy 125 ProProGlyThrPheSerAlaSerSerSerSerGluGlnCysGlnProHisArgAsn 144
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Db 529 CCAATGGGTTCTTCTCAATGAGACGCTCACTTAAGCACCCCTGTAAACACACAAAT 588  
Qy 145 CyethralaleuGllyleuAlaleuAsnValProGlySerSerHisaePThrLeuCyS 164  
Db 589 TGCAGTCTCTTGTGTCCTCCGCTAAGCAGAAAGAAATGCACACGACACATATA--- 645  
Qy 165 ThSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182  
Db 646 -----TGTTCCGGAACAGTGAATCACTCAAAATGTGGAATAGATTGTTACCCCTGT 699  
Qy 183 GluArgAlaValIleAspPhe 189  
Db 700 GAGAGGCAATCTTCAGGTTT 720  
RESULT 6  
US-08-795-445A-5  
; Sequence 5, Application US/08795445A  
; Patent No. 6284485  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehaven Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,445A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1355 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 94..1296  
; US-08-795-445A-5  
Alignment Scores:  
Pred. No.: 3.05e-26 Length: 1355  
Score: 440.50 Matches: 77  
Percent Similarity: 57.75% Conservative: 31  
Best Local Similarity: 41.18% Mismatches: 74  
Query Match: 29.54% Indels: 5  
DB: 4 Gaps: 2  
US-09-936-024-1 (1-271) x US-08-795-445A-5 (1-1355)  
Qy 5 ProThrTyPProTPaGAsPaAlaGluThrGlyLArgLeuValCySAlaGluCysPro 24  
Db 169 CCAAGTACCTTCATTATGACGAAAGAAACCTCTCATCAGCTGTGTGTGACAAATGTCCT 228

Qy 25 ProGlyThrPheValGlnArgProCySArgArgAspSerProThrThrCysGlyProCyS 44  
Db 229 CCGTGACTACCTAAACAAACAACTGTACGCAAGTGAAAGACCGGTGCGCCCTTGC 288  
Qy 45 ProProArgHisTyrThrGlnPheTTPAsnTyrLeuGluArgCySArgTyrCySAsnVal 64  
Db 289 CCGACCACTACACACAGACAGCTGGCACACGACGATGTCTATATCTCAGGCC 348  
Qy 65 LeuCyGluGluArgGluGluGluAlaArgAlaCySHisAlaThrHisAsnArgAlaCyS 84  
Db 349 GTGTGCAAGAGCTGCAGTACGTCAAGACGAGTGCATGTGCCACCAACCCGCTGTGC 408  
Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104  
Db 409 GAATGCAAGAGAGGGCGCTACCTTGAGATGAGATTCTGCTGAACATATAGAGCTGCTC 468  
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCyS 124  
Db 469 CCGGATTTGAGTGTGTCGAACTGGAAACCCAGACGGAATACAGTTTGCAAAAGATGT 528  
Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGluGlnCysGlnProHisArgAsn 144  
Db 529 CCAATGGGTTCTTCTCAATGAGACGCTCATCTTAAGCACCCCTGTGAAACACACAAAT 588  
Qy 145 CyethralaleuGllyleuAlaleuAsnValProGlySerSerSerHisaePThrLeuCyS 164  
Db 589 TGCAGTCTCTTGTGTCCTCCGCTAAGCAGAAAGAAATGCACACGACACATATA--- 645  
Qy 165 ThSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182  
Db 646 -----TGTTCCGGAACAGTGAATCACTCAAAATGTGGAATAGATTGTTACCCCTGT 699  
Qy 183 GluArgAlaValIleAspPhe 189  
Db 700 GAGAGGCAATCTTCAGGTTT 720  
RESULT 7  
US-08-795-447A-5  
; Sequence 5, Application US/08795447A  
; Patent No. 6284728  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Amgen Inc.  
; STREET: One Amgen Center Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91362-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,447A  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378D2  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1355 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear



QY 183 GluArgAlaValIleasphe 189  
 DB 700 GAGAGGCAATCTTCAGGTTT 720

# RESULT 9

US-08-795-446B-5  
 ; Sequence 5, Application US/08795446B  
 ; Patent No. 6288032  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boyle, William J.  
 ; APPLICANT: Lacey, David L.  
 ; APPLICANT: Calzone, Frank J.  
 ; APPLICANT: Chang, Ming-Shi  
 ; TITLE OF INVENTION: OSTEOPROTEGERIN  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Amgen Inc.  
 ; STREET: 1840 Dehavenland Drive  
 ; CITY: Thousand Oaks  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 91320-1789  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/795,446B  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/577,788  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winter, Robert B.  
 ; REFERENCE/DOCKET NUMBER: A-378  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1355 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 94..1296  
 ; US-08-795-446B-5

Alignment Scores:  
 Pred. No.: 3.05e-26 Length: 1355  
 Score: 440.50 Matches: 77  
 Percent Similarity: 57.75% Conservative: 31  
 Best Local Similarity: 41.18% Mismatches: 74  
 Query Match: 29.54% Indels: 5  
 Gaps: 2

US-09-936-024-1 (1-271) x US-08-795-446B-5 (1-1355)

QY 5 ProthThyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24  
 DB 169 CCAAGAGTACCTTCATTATGACGAAGAACTCTCATCAGCTGTGTGTGACAAATGTCCT 228  
 QY 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44  
 DB 229 CCTGGTACCTACTAAACAACACTGTACAGCAAGTGAAGACCGTGTGGCCCTTGC 288  
 QY 45 ProProArgHisIstYrThrGlnPheTrpAsnTyrLeuGlnArgCysArgTyrCysAsnVal 64  
 DB 289 CTTACACCACTACTACAGACAGCTGGACACCACTGACGAGTCTATATCTGACAGCC 348  
 QY 65 LeucCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84

DB 349 GTGTGCAGAGGAGCTGCAGTACGTCAAGCAGAGTGCATGCAACCCAGCCGCTGTGC 408  
 QY 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnIstHisAlaSerCysPro 104  
 DB 409 GAATGCAGAGGAAGGGCGGCTTCTTGAGATGAGTTCCTGCTTGAACATGTGAGACTCCCT 468  
 QY 105 ProGlyAlaGlyValIleAlaPArgGlyThrProSerGlnAsnThrGlnCysGlnProCys 124  
 DB 469 CTGTGATTTGAGTGTGTGACAGTGAACCCAGACCGAAATACATTTGCCAAATGTG 528  
 QY 125 ProProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSerSerSerSerSer 144  
 DB 529 CCAGATGGGTTCTTCTCAATGAGACGTGATCTTAAGACACCTGTAGAAAACACACAAAT 588  
 QY 145 CysThrAlaLeuGlyLeuAlaLeuAlaValProGlySerSerSerSerSerSerSerSer 164  
 DB 589 TGCAGTGTCTTGTCTCTCTGCTTAACTCAGAAAGAAAGCAACACACGACACATTA--- 645  
 QY 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182  
 DB 646 -----TGTTCGGGAACAGTGAATCACTCAAAATGTGAAATAGATGTACCTGTGT 659

# RESULT 10

US-08-706-945D-127  
 ; Sequence 127, Application US/08706945D  
 ; Patent No. 6369027  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boyle, William  
 ; APPLICANT: Lacey, David  
 ; APPLICANT: Calzone, Frank  
 ; APPLICANT: Chang, Ming-Shi  
 ; TITLE OF INVENTION: Osteoprotegerin  
 ; FILE REFERENCE: A-378CIP  
 ; CURRENT APPLICATION NUMBER: US/08/706,945D  
 ; CURRENT FILING DATE: 1996-09-03  
 ; PRIOR APPLICATION NUMBER: 08/577,788  
 ; PRIOR FILING DATE: 1995-12-22  
 ; NUMBER OF SEQ ID NOS: 145  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 127  
 ; LENGTH: 1355  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (94)..(1296)  
 ; OTHER INFORMATION:  
 ; US-08-706-945D-127

Alignment Scores:  
 Pred. No.: 3.05e-26 Length: 1355  
 Score: 440.50 Matches: 77  
 Percent Similarity: 57.75% Conservative: 31  
 Best Local Similarity: 41.18% Mismatches: 74  
 Query Match: 29.54% Indels: 5  
 Gaps: 2

US-09-936-024-1 (1-271) x US-08-706-945D-127 (1-1355)

QY 5 ProthThyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24  
 DB 169 CCAAGAGTACCTTCATTATGACGAAGAACTCTCATCAGCTGTGTGTGACAAATGTCCT 228  
 QY 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44  
 DB 229 CCTGGTACCTACTAAACAACACTGTACAGCAAGTGAAGACCGTGTGGCCCTTGC 288  
 QY 45 ProProArgHisIstYrThrGlnPheTrpAsnTyrLeuGlnArgCysArgTyrCysAsnVal 64

Db	289		:::	:::	:::		:::	348
Qy	65	Leu	CysGly	Glu	Arg	Glu	Glu	84
Db	349	GTGTG	CAGGAG	CTG	CAGT	AGT	CTCA	408
Qy	85	Arg	Cys	Arg	Thr	Gly	Phe	104
Db	409	GAATG	CAAGG	AGG	CGCT	ACCT	TGAG	468
Qy	105	Pro	Gly	Ala	Gly	Val	Ile	124
Db	469	CCTGG	ATTG	TGAG	TGT	GTG	TTG	528
Qy	125	Pro	Pro	Gly	Thr	Phe	Ser	144
Db	529	CCAGAT	GGT	TTCT	CAAA	TGAG	ATG	588
Qy	145	Cys	Thr	Ala	Leu	Gly	Leu	164
Db	589	TGCAG	TGCT	TTT	GTG	TCT	CTG	645
Qy	165	Thr	Ser	Cys	Thr	Gly	Phe	182
Db	646	-----	TG	TCCG	GAAC	AGT	GAAT	699
Qy	183	Glu	Arg	Ala	Val	Ile	Asp	
Db	700	GAGG	AGC	ATT	TTCT	TTC	CAGG	720

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RESULT 11
US-08-997-918-47
; Sequence 47, Application US/08997918
; Patent No. 6077689
; GENERAL INFORMATION:
; APPLICANT: Snively, Marshall D.
; TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS
; FILE REFERENCE: A-496
; CURRENT APPLICATION NUMBER: US/08/997,918
; CURRENT FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: fragment encoding amino acids 22-194 of human OPG
US-08-997-918-47

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Alignment Scores:		
Pred. No.:	3,256-26	Length:
Score:	433.00	Matches:
Percent Similarity:	60.87%	Conservative:
Best Local Similarity:	42.86%	Mismatches:
Query Match:	29.04%	Indels:
DB:	3	Gaps:
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		0

US-09-936-024-1 (1-271) x US-08-997-918-47 (1-525)

Qy	5	ProThrTyrProTrpArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro	24
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Db	16	CCTAAATATCTTCATTATGATGAAGAAACTAGTCACCACTGCTGTGGACAATAATGCTCT	75
Qy	25	ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys	44
		:::::	:::::
Db	76	CCGGTGTAACCTACCTGAAACAGACACTGCACCGCTAATGGAAAACCGTTTGGCGTCTCTGT	135
Qy	45	ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal	64
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Db	136	CCGACCACATCTATACACCGACTCCTGGCACCTCCGCAATGCCCTGACTGCTCATCCG	195
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Percent Similarity: 55.61% Conservative: 33  
 Best Local Similarity: 39.51% Matches: 86  
 Query Match: 28.54% Indels: 5  
 DB: 3 Gaps: 2

US-09-936-024-1 (1-271) x US-08-974-022-1 (1-2432)

Qy 5 ProThrTyPrProTPaAgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24  
 Db 199 CCAAAATACCTTGCTTATGAGCCGAGAAACCGAGCTGCTGTTGTGTGCAAAATGTGCT 258  
 Qy 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44  
 Db 259 CCTGGCAGCTTAAACAGCACTGACAGTCAAGAGAGAACAGACAGTGTGCTCCCTTGC 318  
 Qy 45 ProProArgHisTyrrThrGlnPheTrpAsnTyrrLeuGlnArgCysArgTyrrCysAsnVal 64  
 Db 319 CCTGACTACTCTTATTAACAGACAGCTGGACACGAGTATGATGATGCTGTACTGAGCCCC 378  
 Qy 65 LeuCyseGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84  
 Db 379 GTGTGCAAGAACTGACAGCCGTGAACAGAGTGCACCCGACCCACAGAGTGTGC 438  
 Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHisAlaSerCysPro 104  
 Db 439 GAATGTAGAGAAAGGCGCTACCTGAGCTCGAATTTGCTTGAAGACACCGAGCTGTCCC 498  
 Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124  
 Db 499 CCAGGCTTGGTGTGCTGACAGCTGGAGCCCAAGAGCAACAGCTTTGCAAAAGATGT 558  
 Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerGlnGlnCysGlnProHisArgAsn 144  
 Db 559 CCGATGAGGTTCTTCTAGAGTGAACGTCATCGAAGACCCCTGAGAAACACACCAAC 618  
 Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164  
 Db 619 TGCAGCTCACTGGCTCTCTGCTATTCAGAAAGAAATGCAACACATGACAAATGTA--- 675  
 Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182  
 Db 676 -----TGTTCGGGAAACAGAAAGCACTCAAAATTTGTGGAATGATGTCACCCCTGTGC 729  
 Qy 183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg 202  
 Db 730 GAAGAGCATTTCTCAGGTTTCTGTGCTTACCAAGATTATACCAATTGAGTGTGTT 789  
 Qy 203 LeuLeuGlnAlaLeu 207  
 Db 790 CTGGTGACAGTTTG 804  
 RESULT 13  
 US-08-795-445A-1  
 : Sequence 1, Application US/08795445A  
 : Patent No. 6284485  
 : GENERAL INFORMATION:  
 : APPLICANT: Boyle, William J.  
 : APPLICANT: Lacey, David L.  
 : APPLICANT: Calzone, Frank J.  
 : APPLICANT: Chang, Ming-Shi  
 : TITLE OF INVENTION: OSTEOPROTEGERIN  
 : NUMBER OF SEQUENCES: 53  
 : CORRESPONDENCE ADDRESSES:  
 : ADDRESSEE: Amgen Inc.  
 : STREET: 1840 Dehavenland Drive  
 : CITY: Thousand Oaks  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 91320-1789  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/795,445A  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/577,788  
 : FILING DATE:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Winter, Robert B.  
 : REFERENCE/DOCKET NUMBER: A-378  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 2432 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: 124..1326  
 : US-08-795-445A-1

Alignment Scores:  
 Pred. No.: 1,06e-24 Length: 2432  
 Score: 425.50 Matches: 81  
 Percent Similarity: 55.61% Conservative: 33  
 Best Local Similarity: 39.51% Mismatches: 86  
 Query Match: 28.54% Indels: 5  
 DB: 4 Gaps: 2

US-09-936-024-1 (1-271) x US-08-795-445A-1 (1-2432)

Qy 5 ProThrTyPrProTPaAgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24  
 Db 199 CCAAAATACCTTGCTTATGAGCCGAGAAACCGAGCTGCTGTTGTGTGCAAAATGTGCT 258  
 Qy 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCysGlyProCys 44  
 Db 259 CCTGGCAGCTTAAACAGCACTGACAGTCAAGAGAGAACAGACAGTGTGCTCCCTTGC 318  
 Qy 45 ProProArgHisTyrrThrGlnPheTrpAsnTyrrLeuGlnArgCysArgTyrrCysAsnVal 64  
 Db 319 CCTGACTACTCTTATTAACAGACAGCTGGACACAGAGTATGATGATGCTGTACTGAGCCCC 378  
 Qy 65 LeuCyseGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84  
 Db 379 GTGTGCAAGAACTGACAGCCGTGAACAGAGTGCACCCGACCCACAGAGTGTGC 438  
 Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHisAlaSerCysPro 104  
 Db 439 GAATGTAGAGAAAGGCGCTACCTGAGCTCGAATTTGCTTGAAGACACCGAGCTGTCCC 498  
 Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124  
 Db 499 CCGAGCTTGGTGTGCTGCTGACAGCTGGAGCCCGAGAGAAACACGCTTTGCAAAAGATGT 558  
 Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerGlnGlnCysGlnProHisArgAsn 144  
 Db 559 CCGATGAGGTTCTTCTCAGGTGAGACGTCATCGAAGACACCTGTAGAGAAACACACCAAC 618  
 Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164  
 Db 619 TGCAGCTCACTGGCTCTCTGCTATTCAGAAAGAAATGCAACACATGTAATGTA--- 675  
 Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182  
 Db 676 -----TGTTCGGGAAACAGAAAGCACTCAAAATTTGTGGAATGATGTCACCCCTGTGC 729  
 Qy 183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeuGlnArg 202  
 Db 730 GAAGAGCATTTCTCAGGTTTGTGCTTACCAAGATTATACCAATTGAGTGTGTT 789

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QY 203 LeuLeuGlnAlaLeu 207
Db 790 CTGGTGACAGTTTG 804

RESULT 14
US-08-795-447A-1
; Sequence 1, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1326
US-08-795-447A-1

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; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 124..1326
US-08-974-186-1

Alignment Scores:

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GenCore version 5.1.3  
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Listing first 45 summaries

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SUMMARIES

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6	1491	100.0	1550	10	US-09-935-727-33	Sequence 33, Appl
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8	1339	89.8	1859	10	US-09-877-156-19	Sequence 19, Appl
9	1287.5	86.4	1796	10	US-09-935-727-28	Sequence 28, Appl
10	982.5	65.9	1667	10	US-09-935-727-3	Sequence 3, Appl
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20	440.5	29.5	1089	10	US-09-062-113-10	Sequence 10, Appl
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ALIGNMENTS

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; Patent No. US20020150583A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PP454P2  
; CURRENT APPLICATION NUMBER: US/09/935,727  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/227,598  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: 09/518,931  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: 60/168,235  
; PRIOR FILING DATE: 1999-12-01  
; PRIOR APPLICATION NUMBER: 60/146,371  
; PRIOR FILING DATE: 1999-08-02  
; PRIOR APPLICATION NUMBER: 60/131,964  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: 60/131,270  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/124,092  
; PRIOR FILING DATE: 1999-03-12



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GENERAL INFORMATION:			
APPLICANT: ASHKENAZI, AVI J			
APPLICANT: BOTSSTEIN, DAVID			
APPLICANT: DODGE, KELLY H.			
APPLICANT: GURNEY, AUSTIN L.			
APPLICANT: KIM, KYUNG JIN			
APPLICANT: LAWRENCE, DAVID A.			
APPLICANT: PITTI, ROBERT			
APPLICANT: ROY, MARGARET A			
APPLICANT: TOMAS, DANIEL B			
APPLICANT: WOOD, WILLIAM I.			
TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog			
FILE REFERENCE: P134R2 REVISED			
CURRENT APPLICATION NUMBER: US/09/896,096A			
CURRENT FILING DATE: 2001-06-28			
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PRIOR FILING DATE: 1998-09-18			
PRIOR APPLICATION NUMBER: US 60/059,288			
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PRIOR FILING DATE: 1998-07-30			
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; GENERAL INFORMATION:			
; APPLICANT: Human Genome Sciences, Inc.			
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta			
; FILE REFERENCE: PF454P2			
; CURRENT APPLICATION NUMBER: US/09/935,727			
; CURRENT FILING DATE: 2001-08-24			
; PRIOR APPLICATION NUMBER: 60/303,224			
; PRIOR FILING DATE: 2001-07-06			
; PRIOR APPLICATION NUMBER: 60/252,131			
; PRIOR FILING DATE: 2000-11-21			
; PRIOR APPLICATION NUMBER: 60/227,598			
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; PRIOR APPLICATION NUMBER: 60/131,964			
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; PRIOR APPLICATION NUMBER: 60/131,270			
; PRIOR FILING DATE: 1999-04-27			
; PRIOR APPLICATION NUMBER: 60/124,092			
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: PRIOR FILING DATE: 1999-03-04									
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: PRIOR FILING DATE: 1997-01-14									
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Db	1218	GAATCTTGTCATCTCTGTGTACTGTGTTTCTTGTCTACTAGAGGTTCCAGGTGCTGAA	1277						
Qy	181	GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleYsArgLeu	200						
Db	1278	GAAATGTAAGAGCTGTATATGATTTTGTGCTTTTCAAGATATTTCTATTTAAGAGCTG	1337						
Qy	201	GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTTPGlyProThrProArgAlaGly	220						
Db	1338	CAAAAGATGCTGCACACTCGAAGCTCCAGAAAGGTGGGGTCCAACTCCAAGAGCTGT	1397						
Qy	221	ArgAlaAlaLeuGlnLeuIysLeuArgAlaGlyLeuThrGlnLeuLeuGlyValaGlnAsp	240						
Db	1398	AGAGCTGCTTGTGAATTTGAATTTGAAGAAAGAAATTTGACGAATTTTGTGGGTCCAAAT	1457						





Db 285 TGTGCCCCGTGTCACCGCGCCACTACAGCAGGTTCTGGAACTACTGAGAGCGTGC 344  
QY TyrCysAsnValLeuCYsGlyGlyuArgGlyuArgAlaCYsHisAlaThrHis 80  
Db 345 TACTGCACAGCTCTCTGCGGGAGGCTGAGAGAGAGCAGGAGCTTGCACAGCCAC 404  
QY AsnArgAlaCYsArgCYsArgThrGlyPhePheAlaHisAlaGlyPheCYsLeuGlyHis 100  
Db 405 AACGGTGGCTCGCGCTGCGCAGCGGCTTCTTCCGCGCAGCGTGGTTCTGCTGAGAG 464  
QY AlaSerCYsProProGlyAlaGlyValIleAlaProGlyThrProSerGlyAsnThrGln 120  
Db 465 GCATCTGTCTCACCCTGCTGCGCGCTGATGCTCCCGGCGACCCCGCAGAACACG 524  
QY CysGlnProCYsProProGlyThrPheSerAlaSerSerSerSerGlyGlnCYsGln 140  
Db 525 TGCCAGCGCTGCCCCCGCAGGACCTTCTCAGCCACAGCTTCAGAGCAGTGCAG 584  
QY ProHisArgAsnCYsThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160  
Db 585 CCCACCGCAACTGACGCGCTGGGCTGGGCTCAATGTCAGAGCTCTTCTCCCAT 644  
QY AspThrLeuCYsThrSerCYsThrGlyPheProLeuSerThrArgValPro----- 177  
Db 645 GACACCCCTGTGACACGCTGACGTGCTTCCCTCCACAGCAGGAGTACAGTGAGCA 704  
QY 177 ----- 177  
Db 705 GAGGCTGAGGGGAGACACACTGAGGCGCAGCCACTTGTGCCCTCACTCTGCCCT 764  
QY 177 ----- 177  
Db 765 GCAGGTGATCTAGGCTGAGGAGTCCAGTGGCTTGGGAAAGGGGCCACAGTGGATTG 824  
QY 177 ----- 177  
Db 825 AGGGGTGAGGGGTCCCTCCACTAGATCCCAACAAGTCTGCCCTCTCAGGGGTGGCTGAG 884  
QY 177 ----- 177  
Db 885 AATTTCGATCTGAGCCAGGAGGACAGCTCCCTCGAGAGCTCTGGGAAAGTGGCAGCA 944  
QY 177 ----- 177  
Db 945 TCTCTAACTGCCGAGGGGAAAGTGGCTGCTCTGACACGGGGAAACCGAGGCTG 1004  
QY 177 ----- 177  
Db 1005 ATGTGAATTCTCTAACTGCTGAGAGGAAAGTGGCTGCTCTCTGACATGGGAAAC 1064  
QY 177 ----- 177  
Db 1065 GAGGCCAATGTAACTGCTGTGAGAAAGTACAGAGGGGAAAGTACCCCTTAACTCA 1124  
QY 177 ----- 177  
Db 1125 GTCAAGTCCGCTCATCTGACAGTCCCAACTGCCCTTCCGATGGCCAGAGAGCCCA 1184  
QY 177 ----- 177  
Db 1185 GCCCTTGGCTGGGCCCCCTTGCCTCTTTCAGCAAGAGTCCGATGGCGCTCTGCCCC 1244  
QY 177 ----- 177  
Db 1245 TAGGCTTTGCTCCAGCTCTGTGACCAAGGCTCTGCTCTCCAGTCCCATGCTT 1304  
QY 177 ----- 177  
Db 1305 GCACGTGCTTCCAGAGCGGCTCACTGACAGAGGATTTCTCTCTGCAAAACCCCGG 1364  
QY 177 ----- 177

Db 1365 AGTGGGGCCAGAAAGAGGTACTGTCAGACCCCGCCCACTGTGTGTGGTGAATGAT 1424  
QY 178 -----GlyAlaGlyuGlyGlyuArgAlaValIleAs 188  
Db 1425 CGGACCGCTGCTCCCAACCCACTGACAGAGCTTGAAGAGTGAAGGTGCTGATCGA 1484  
QY 188 pPheValAlaPheGlnAspIleSerIleYsArgLeuGlnArgLeuGlnAlaLeuG 208  
Db 1485 CTTGTGGCTTCCAGGACATCTCATCAAGAGCTCAGCGGCTGCTGACAGGCTCGA 1544  
QY 208 uAlaProGlyGlyThrGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeu 228  
Db 1545 GGGCCCGAGGGCTGGGGTGCAGACCAAGGCGGCGGCTTGCAGCTGAAGCT 1604  
QY 228 uArgArgArgLeuThrGlyLeuLeuGlyValAlaAspGlyValaLeuLeuValArgLeu 248  
Db 1605 GCGTGGCGGCTTCCAGAGCTCTTGGGAGGCGCAGAGAGGGCGTGGTGGCGGCTG 1664  
QY 248 uGlnAlaLeuArgValAlaArgMetProGlyLeuGlyuArgSerValArgGluArgPhe 268  
Db 1665 GCAGGCGCTGCGCTGGCCAGAGTCCCGGCTGGAGCGGAGCTCCGTAGCGCTTCT 1724  
QY 268 uProValHis 271  
Db 1725 CCTGTGTCAC 1734  
RESULT 9  
US-09-935-727-28  
Sequence 28, Application US/09935727  
Patent No. US20020150583A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
FILE REFERENCE: P454P2  
CURRENT APPLICATION NUMBER: US/09/935,727  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 60/303,224  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: 60/252,131  
PRIOR FILING DATE: 2000-11-21  
PRIOR APPLICATION NUMBER: 60/227,598  
PRIOR FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: 09/518,931  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/168,235  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 60/146,371  
PRIOR FILING DATE: 1999-08-02  
PRIOR APPLICATION NUMBER: 60/131,964  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: 60/131,270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/124,092  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/121,774  
PRIOR FILING DATE: 1999-03-04  
PRIOR APPLICATION NUMBER: 09/006,352  
PRIOR FILING DATE: 1998-01-13  
PRIOR APPLICATION NUMBER: 60/035,496  
PRIOR FILING DATE: 1997-01-14  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 1796  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: intron  
LOCATION: 425-560  
NAME/KEY: intron  
LOCATION: 756-1512  
US-09-935-727-28



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; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)..(582)
US-09-935-727-3

Alignment Scores:
Pred. No.: 66-67      Length: 1667
Score: 982.50      Matches: 179
Percent Similarity: 78.85%      Conservative: 0
Best Local Similarity: 78.85%      Mismatches: 2
Query Match: 65.90%      Indels: 46
                        Gaps: 1

US-09-936-024-1 (1-271) x US-09-935-727-3 (1-1667)
QY 1 ValAlaGluThrProThrTyrProTrrPaRgAspAlaGluThrGlyGluArgLeuValCys 20
Db 160 GTGCGAGAAACACCACCTACCCCTGCGGGAGCGAGAGACAGGAGGAGCGGCTGGTGTGC 219
QY 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgSerProThrThr 40
Db 220 GCCCAGTGTCCCCCAGGACCTTGTGTGACGGCGCTGCCGCCAGACAGCCCAACGACG 279
QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrrPanTyrLeuGluArgCysArg 60
Db 280 TGTGGCCCTGTCCACCGCGCACCTACACGCACTTCTGAACTTCTGAGGCGCTGGCCGC 339
QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluArgAlaCysHisAlaThrHis 80
Db 340 TACTGCAACGTCCTCTGCGGGAGCGTGAGAGAGACAGGCGGCTTGCACGCCACCCAC 399
QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 400 AACCGTCTCCCTGCGTCCGACCGGCTTCTTCCGCGCACGCTGTGTTCTGCTTGGAGCAC 459
QY 101 AlaSerCysProProGlyAlaGlyValIleAlaPro----- 112
Db 460 GCATGTGTCCACCTGTGCGGCGCTGATGTGCCCGGGGTGAGAGCTGGGCGAGGGGAGGG 519
QY 112 ----- 112
Db 520 GCCCCAGAGAGTGTGGCCGAGAGGTGTGGCAGGGGTCAAGTTGCTGTCCACAGCTTGA 579
QY 113 -----GlyThrPr 115
Db 580 CCTGAGCTAGACACACGATTCCTCCCTGACCTTCTTCCCTGCTGAGGAGGACCC 639
QY 115 cSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSe 135
Db 640 CAGCCAGAAACAGCAGTGTCCAGCCCTGCGCCCAAGCACTTCTTACGCCAGCAGCTTCAG 699
QY 135 rSerGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPr 155
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Db 700 CTCAGACAGTGTCCAGGCCCAACCGCAACTGCACAGCCCTGGGCTGTCCATATGTGCC 759
QY 155 oGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrAr 175
Db 760 AGGCTTCTTCTCCCATATACACCTGTGTACACAGCTGTGACCTTCCCTCAGACACAG 819
QY 175 gValProGlyAlaGluGlu 181
Db 820 GGTACCAAGGTGACCCAGAG 838

RESULT 11
US-09-896-096A-3
; Sequence 3, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROT, MARGARET A
; APPLICANT: TOMAS, DANIEL B.
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unknown organism
; NAME/KEY: unsure
; LOCATION: 62, 73, 86, 98
; OTHER INFORMATION: unknown base
US-09-896-096A-3

Alignment Scores:
Pred. No.: 4,786-58      Length: 491
Score: 858.00      Matches: 156
Percent Similarity: 95.71%      Conservative: 0
Best Local Similarity: 95.71%      Mismatches: 6
Query Match: 57.55%      Indels: 1
                        Gaps: 0

US-09-936-024-1 (1-271) x US-09-896-096A-3 (1-491)
QY 35 ArgAspSerProThrTyrCysGlyProCysProProArgHisTyrThrGlnPheTrrPan 54
Db 3 CGAGACAGCCCAACGAGTGTGGCCGCTGTCCACCGCGCACCTACAGCAGGATTTGGAAN 62
QY 55 TyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluArgAlaArg 74
Db 63 TAACTGAGCNCCTGCGCTCTAGTGAACGTCTCTGNGGGAGGCGTGAAGAGGACGG 122
QY 75 AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAla 94
Db 123 GCTTGCACAGCAGCAACCAACCGTGTGCGGCTGCGGACCGGCTTCTTGGGCAAGCT 182
QY 95 GlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThr 114
Db 183 GGTTCGTGCTTGGAGCAGCATCGTGTCCACCTGTGCGCGCGGTGATGGCCCGGGAGCC 242
|||||
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Db 181 AGCCAGAACACGAGTGCACCGCTGCCCCCAAGGACCTTCTCAGGCACAGCTCCAGC 240
Qy 136 SerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValPro 155
Db 241 TCAGAGCAGAGCCAGCCGACCCGCACTGACGCGCTGGGCTGGGCTCCCAATGGGCCA 300
Qy 156 GlycerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArg 175
Db 301 GGCTCTTCTCCCTCATGACACCTCTGTGACACGCTGCTGCTTCCCCCTCAGACCCAG 360
Qy 176 ValProGlyAlaGluGlnCysGluArgAlaValIleAspPheValAlaPheGlnAspIle 195
Db 361 GTACCAAGAGCTGAGAGTGTGAGCGCTGACCTGATCGACTTGTGGCTTCCAGACATC 420
Qy 196 SerIleValArgLeuGlnArgLeuLeuGlnAlaLeuGln 208
Db 421 TCATCAAGAGCTGACGCGCTGCTGACGCGCTCCAG 459

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## RESULT 14

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US-09-062-113-92
Sequence 92, Application US/09062113
Patent No. US20020051969A1
GENERAL INFORMATION:
APPLICANT: GOTO, Masaki
APPLICANT: TSUDA, Eisuke
APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: KOBAYASHI, Fumie
APPLICANT: SHIMA, No. US20020051969A1uyuki
APPLICANT: YASUDA, Hisataka
APPLICANT: NAKAGAWA, No. US20020051969A1uaki
APPLICANT: MORINAGA, Tomonori
APPLICANT: UEDA, Masatsugu
APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault
STREET: 125 High St.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
FILING DATE: 17-APR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
FILING DATE: 20-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, Ronda P. 44,244
REGISTRATION NUMBER: 44,244
REFERENCE/DOCKET NUMBER: FCN-060DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100

```

```

; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..981
; OTHER INFORMATION: /note= "(OC1F-DDD1)".
US-09-062-113-92
Alignment Scores:
Pred. No.: 2,81e-27 Length: 981
Score: 461.00 Matches: 94
Percent Similarity: 53.178 Conservative: 57
Best Local Similarity: 33.104 Mismatches: 101
Query Match: 30.924 Indels: 32
DB: Gaps: 7

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US-09-936-024-1 (1-271) x US-09-062-113-92 (1-981)

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Qy 5 ProThrTyProTPrArgAspAlaGluThrGlyGluArgLeuValCysAlaGlnCysPro 24
Db 76 CCAAGTACCTTCATTATATGACGAAGAACTCTCATCAGCTGTGTGTGACAAATGCTCT 135
Qy 25 ProGlyThrPheValGlnArgProCysArgArgAspSerProThrCysGlyProCys 44
Db 136 CCGTGATCCTTCACTAAACCAACCTGTACAGCAAGTGAAGACCGTGCGCCCTTGC 195
Qy 45 ProProArgHisThrThrGlnPheThrPheThrPheThrLeuGlnArgCysArgTyCysAsnVal 64
Db 196 CCGTACCACTTACTACACAGACAGCTGGACACACAGTACAGTGTCTATCTGACGCC 255
Qy 65 LeuCysGlyGluArgGluGlnGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84
Db 256 GTGTGCAAGAGAGCTGACGTACGTCAAGCAGAGTGCATGACGCCACCAACCGGTGTGC 315
Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlnHisAlaSerCysPro 104
Db 316 GAATGCAAGAGAGGCGCTGCTTGAATGAGTTCCTTGAACCTAGAGCTGCGCT 375
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124
Db 376 CCGGATTTGGAGTGGTCAAGCTGGAACTCCAGAGCAATACAGTTTGCATAAAGATGT 435
Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerSerGlnGlnCysGlnProHisArgAsn 144
Db 436 CCAGATGGGCTTCTTCAATAGACACTCATCTAAGACACCTGTAGAAAACACACAAT 495
Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164
Db 496 TGCAGTGTCTTGTCTCCGTCTAAGTCAAGAAAGAAATCAACACACGACCAACATA 552
Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGly-----AlaGluGlnCys 182
Db 553 -----TGTCCGGAACACGTGAATCACTCAAAATGTGAATGATTGACTCTGT 606
Qy 183 GluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleValArgLeuGlnArg 202
Db 607 GAAAACAGCGTGCAGCGGCACATTGGACATGCACTCACTCCTTGCAGACGCTTGTGAGC 666
Qy 203 LeuLeuGlnAlaLeuGlnAlaProGlnGlyTyrGlyProThrProArgAlaGlyArgAla 222
Db 667 TTGATGGAAGCTTA-----CCGGGAAGAAAGTGGGAGCGAAG 705
Qy 223 AlaLeuGlnLeuValSerLeuArgArg-----ArgLeuThrGlnLeuLeu--- 236
Db 706 GACATTGAAAAAACATTAAGGATGCAAAACCAAGTGCACCAAGTCTGGAAGCTGTGACT 765
Qy 237 -----GlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAla 250

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Db 766 TTGTGGCGAATAAATAATGGGACCAAGAC-----ACCTTGAAGGCGCTAATGCCAGCA 819  
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Db 820 CTAAGCACTCAAGAGCTACCACTTTCCCAAACTGTCTCAGAGTCTAAAGAGACC 879  
Qy 266 ---ArgPheLeu 268  
Db 880 ATCAGGTTCTT 891

## RESULT 15

US-09-062-113-83  
; Sequence 83, Application US/09062113  
; Patent No. US20020051969A1  
; GENERAL INFORMATION:  
; APPLICANT: GOTO, Masaaki  
; APPLICANT: TSUDA, Eisuke  
; APPLICANT: MOCHIZUKI, Shin'ichi  
; APPLICANT: YANO, Kazuki  
; APPLICANT: KOBAYASHI, Fumie  
; APPLICANT: SHIMA, No. US20020051969A1uyuki  
; APPLICANT: YASUDA, Hisataka  
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki  
; APPLICANT: MORINAGA, Tomonori  
; APPLICANT: UEDA, Masatsugu  
; APPLICANT: HIGASHIO, Kanji  
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing  
; TITLE OF INVENTION: the Proteins  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Testa, Hurwitz & Thibault  
; STREET: 125 High St.  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/062,113  
; FILING DATE: 17-APR-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 54977/1995  
; FILING DATE: 20-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 207508/1995  
; FILING DATE: 21-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP96/00374  
; FILING DATE: 20-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,004  
; FILING DATE: 20-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MOORE, Ronda P.  
; REGISTRATION NUMBER: 44,244  
; REFERENCE/DOCKET NUMBER: FJN-060DV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1206 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE: -  
; NAME/KEY: -

; LOCATION: 1..1206  
; OTHER INFORMATION: /note= "(OCIF-C19S)"  
US-09-062-113-83  
Alignment Scores:  
Pred. No.: 9,39e-26 Length: 1206  
Score: 442.50 Matches: 77  
Percent Similarity: 57.75% Conservative: 31  
Best Local Similarity: 41.18% Mismatches: 74  
Query Match: 29,68% Indels: 5  
DB: 10 Gaps: 2

US-09-936-024-1 (1-271) x US-09-062-113-83 (1-1206)

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Db 76 CCNAAGTACTTCATTATGACGAGAAACCTCTCATCTGTTGTGTGACAAATGTCT 135  
Qy 25 ProGlyThrPheValGlnArgProCysArgAspSerProThrThrCysGlyProCys 44  
Db 136 CCTGGTACTACTCTAAACACACTGTACAGCAAAAGTGGAGACCGGTGGCGCCCTTGC 195  
Qy 45 ProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArgTyrCysAsnVal 64  
Db 196 CCTGACCACTACTACACAGACAGCTGGCACACCAAGTGCAGAGTGTCTATACTGCAGCCC 255  
Qy 65 LeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsnArgAlaCys 84  
Db 256 GTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCATCGCACCCACACCGCGTGTGC 315  
Qy 85 ArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAlaSerCysPro 104  
Db 316 GAATGCAAGGAAGGCGCTACCTTGAGATAGAGTTCCTGTTGAAACATAGGAGTGCCT 375  
Qy 105 ProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGlnCysGlnProCys 124  
Db 376 CCTGGATTGGAGTGTGCAAGCTGCAACCCAGAGCGAATAACAGTTTGCAAAAGATGT 435  
Qy 125 ProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGlnProHisArgAsn 144  
Db 436 CCAGATGGGTTCTTCTCAATGAGAGCTCATCTAAGCACCCCTGTAGAAAACACACAAAT 495  
Qy 145 CysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHisAspThrLeuCys 164  
Db 496 TGCAGTGTCTTTGGTCTCTCTGCTAACTCAGAAAGGAATGCAACACACACACACATA--- 552  
Qy 165 ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGluGlu-----Cys 182  
Db 553 -----TGTTCGGAACACAGTGAATCACTCAAAAAAGTGAATAGATGTTACCCCTGTGT 606  
Qy 183 GluArgAlaValIleAspPhe 189  
Db 607 GAGGAGGCATTCTTCAGGTTT 627

Search completed: January 6, 2003, 13:48:04  
Job time : 136 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

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(without alignments)  
8851.695 Million cell updates/sec

Title: US-09-936-024-2  
Perfect score: 813  
Sequence: 1 gtggcagaacaccaccta.....agccttcctccctgtgcac 813

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

GenEmbl:\*

1: gb\_ba:\*

2: gb\_hcg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_stb:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_stb:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_hcg\_hum:\*

31: em\_hcg\_inv:\*

32: em\_hcg\_other:\*

33: em\_hcg\_mus:\*

34: em\_hcg\_pln:\*

35: em\_hcg\_rod:\*

36: em\_hcg\_man:\*

37: em\_hcg\_vrt:\*

38: em\_sy:\*

39: em\_hlgo\_hum:\*

40: em\_hlgo\_mus:\*

41: em\_hlgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	100.0	813	6	AX119833 Sequence
2	813	100.0	813	6	AX167223 Sequence
3	813	100.0	813	6	AX375169 Sequence
4	813	100.0	903	9	AF134240 Homo sapi
5	813	100.0	1048	9	AF217794 Homo sapi
6	813	100.0	1055	6	AX082868 Sequence
7	813	100.0	1114	6	AX055373 Sequence
8	813	100.0	1114	6	AX056645 Sequence
9	813	100.0	1114	9	AF104419 Homo sapi
10	813	100.0	1125	9	BC017065 Homo sapi
11	813	100.0	1168	6	AX017828 Sequence
12	813	100.0	1347	6	AR171895 Sequence
13	813	100.0	1428	9	AF217793 Homo sapi
14	813	100.0	4945	9	AB029011 Homo sapi
15	811.4	99.8	1150	9	BC034349 Homo sapi
16	811.4	99.8	5769	9	HS080248 Homo sapi
17	809.8	99.6	936	6	AX093178 Sequence
18	809.8	99.6	936	6	AX097545 Sequence
19	809.8	99.6	936	6	AX098029 Sequence
20	809.8	99.6	936	6	AX119836 Sequence
21	809.8	99.6	936	6	AX167230 Sequence
22	809.8	99.6	936	6	AX375171 Sequence
23	533.4	65.6	1859	6	AR171896 Sequence
24	459	56.5	459	6	AR171887 Sequence
25	385.8	47.5	120917	9	HSJ583P15 Homo sapi
26	381	46.9	114793	9	AF217796 Homo sapi
27	216.8	26.7	925	6	AX251528 Sequence
28	216.8	26.7	925	6	AX346745 Sequence
29	190.8	23.5	925	6	AX251527 Sequence
30	190.8	23.5	925	6	AX346744 Sequence
31	129.6	15.9	525	6	AR099131 Sequence
32	121	14.9	1116	5	AF401631 Sequence
33	117.8	14.5	1148	5	OMY315137 Sequence
34	112	13.8	2432	6	AR168728 Sequence
35	112	13.8	2432	6	AR205587 Sequence
36	112	13.8	2432	6	AX076604 Sequence
37	112	13.8	2432	10	RM94330 Rattus norv
38	110.4	13.6	1324	6	AR168729 Sequence
39	110.4	13.6	1324	6	AR205588 Sequence
40	110.4	13.6	1325	10	MM094331 Mus muscu
41	108.8	13.4	2818	10	AB013898 Mus muscu
42	107.2	13.2	1325	6	AX076606 Sequence
43	103	12.7	1166	9	AF134187 Homo sapi
44	103	12.7	1206	6	E15271 Human mRNA
45	103	12.7	1206	9	AB002146 Homo sapi

## ALIGNMENTS

RESULT 1	LOCUS	AX119833	813 bp	DNA	linear	PAT 11-MAY-2001
DEFINITION	Sequence 2 from Patent WO0128582.					
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VERSION	AX119833.1	GI:14036593				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Bukaryca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
TITLE	Bumol,T.F. and Cohen,F.U.					
JOURNAL	Therapeutic applications of flint polypeptides					
	Patent: WO 0128582-A 2 26-APR-2001.					





Db	721	GGGGGGCTGCTGTGTCGGGTGCTGCAGGGCGCTGCGGTGGCCAGGATGCCGGGCTGGAG	780
Qy	781	CGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC	813
Db	781	CGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC	813
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DEFINITION	Sequence 2 from Patent WO0209668.		linear
ACCESSION	AX375169		
VERSION	AX375169.1	GI:19169920	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Micanovic, R. and Wiltcher, D.R.		
TITLE	Pulmonary administration of flint		
JOURNAL	Patent: WO 0209668-A 2 07-FEB-2002;		
FEATURES	ELI LILLY AND COMPANY (US)		
source	Location/Qualifiers		
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BASE COUNT	122 a 298 c 267 g 126 t		
ORIGIN			
Query Match	100.0%; Score 813; DB 6; Length 813;		
Best Local Similarity	100.0%; Pred. No. 7e-125;		
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	GTGGAGAAACACCCACTACCCCTGGGGGAGAGAGACAGGGGAGCGGTGTC	60
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Qy	301	GCATGTCCTGTCACCTGATGCGGCGTGAATTGCCCGGGACCCCGACAGCAAGCAG	360
Db	301	GCATGTCCTGTCACCTGATGCGGCGTGAATTGCCCGGGACCCCGACAGCAAGCAG	360
Qy	361	TGCCAGCGGTGCGGCGGCGGACCTTTCTCAGCAGAGAGTCCAGCTCAGAGCAGTCCAG	420
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Qy	421	CCCCACCGCACTGACAGGAGCGTGGGCGTGGCCCAATGTGCCAGAGGCTTTCCTCCAT	480
Db	421	CCCCACCGCACTGACAGGAGCGTGGGCGTGGCCCAATGTGCCAGAGGCTTTCCTCCAT	480
Qy	481	GACACCTGTGTCACAGCTGCACTGGCTTCCCTCAGACAGGAGTACAGAGAGTGGAG	540
Db	481	GACACCTGTGTCACAGCTGCACTGGCTTCCCTCAGACAGGAGTACAGAGAGTGGAG	540
Qy	541	GAGTGTGAGCGTCCGCTCATGCACTTTGTGCTTTTCAGAGACATTCATCAAGAGCTG	600
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Qy	601	CAGGGCGCTGTCAGAGGGCCCTTGAGAGCCCGCCGAGAGGCTTGAGGCTCCGACACACAAAGGCGGGC	660
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Qy	661	CGCGCGGCTTGCAGAGCTGAGCTGAGCTGCGCGGCTCAGCGAGCTCTTGAGGCGCAGGAC	720
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Qy	721	GAGGCGCTGCTGTGTGTGTCGAGGCTGCTGAGGCGCTGCGCGTGGCCAGAGATCCCGGCGTGAAG	780
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Qy	781	CGAGCGCTCGGTGAGCGGCTTCCCTCCCTGTGAC	813
Db	781	CGAGCGCTCGGTGAGCGGCTTCCCTCCCTGTGAC	813
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DEFINITION	Homo sapiens tumor necrosis factor receptor homolog (TR6) mRNA,		
ACCESSION	AF134240		
VERSION	AF134240.1 GI:4768938		
KEYWORDS	Homo sapiens.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1. (bases 1 to 903)		
AUTHORS	Yu, K.Y., Kwon, B., Ni, J., Zhai, Y., Ebner, R. and Kwon, B.S.		
TITLE	A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis		
JOURNAL	J. Biol. Chem. 274 (20), 13733-13736 (1999)		
MEDLINE	99253915		
PUBMED	10318773		
REFERENCE	2. (bases 1 to 903)		
AUTHORS	Kwon, B.S. and Yu, K.Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-MAR-1999) Micro/Immuno1, Indiana University, 635 Barnhill Drive, Indianapolis, IN 46202, USA		
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Query Match	100.0%; Score 813; DB 9; Length 903;		
Best Local Similarity	100.0%; Pred. No. 6, 8e-125;		
Matches 813; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	GTGGCAGAAACACCCACCTACCCCTTGGCGGAGCGCAGACAGAGGAGCGGCTGTGTGC	60
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QY 121 TGTGGCCGCTGTCACCGCGCCACTACACGAGTCTTGGAACTACCTGGAGCGCTGCCGC 180  
Db 208 TGTGGCCGCTGTCACCGCGCCACTACACGAGTCTTGGAACTACCTGGAGCGCTGCCGC 267  
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Db 328 AACCGTGCCTGCCCTGCCGACCGCTTCTTCCGCAACGCTGCTTCTGCTGGAGCAG 387  
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DEFINITION  
ACCESSION AF217794  
VERSION  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM  
REFERENCE 1 (bases 1 to 1048)  
AUTHORS Bai, C., Connolly, B., Metzger, M.L., Hilliard, C.A., Liu, X., Sandig, V., Soderman, A., Galloway, S.M., Liu, Q., Austin, C.P. and Caskey, C.T.  
TITLE Overexpression of M68/Dcr3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)

MEDLINE 20122600  
PUBMED 1065513  
REFERENCE 2 (bases 1 to 1048)  
AUTHORS Bai, C.  
TITLE Direct Submission  
JOURNAL Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories, Summeytown Pike, West Point, PA 19403, USA  
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DB 800 CGCGCGGCTTTCAGAGCTGGAAGCTGCTGGCGGCTTCACGAGAGCTCTGGGGGCGCAGAGC 859
QY 721 GGGGCGCTGCTGGGCGGAGCTGTCAGAGCGCTGGCGGCTTCAGAGAGTCCCGGGCTGGAG 780
DB 860 GGGGCGCTGCTGGGCGGAGCTGTCAGAGCGCTGGCGGCTTCAGAGAGTCCCGGGCTGGAG 919
QY 781 CGGAGCGCTCCGTGAGCGCTTCTCTCTCTGTCAC 813
DB 920 CGGAGCGCTCCGTGAGCGCTTCTCTCTCTGTCAC 952

RESULT 6
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LOCUS Sequence 1 from Patent WO0110908.
ACCESSION AX082868
VERSION AX082868.1 GI:13184802
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Neu, H.
TITLE Neu, H. a member of the tnf-receptor supergene family
JOURNAL Patient: WO 0110908-A 1 15-FEB-2001;
Amgen Inc. (US)
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 813; DB 6; Length 1055;
Best Local Similarity 100.0%; Pred. No. 6, 6e-125;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCAGAAACACCCACTTACCTTGGCGGAGCAGAGAGAGAGGAGCGGCTGTGTGC 60
DB 154 GTGGCAGAAACACCCACTTACCTTGGCGGAGCAGAGAGAGAGAGGAGCGGCTGTGTGC 213
QY 61 GCCCAGTGGCCCCCAGGACCTTGTGTCAGAGCGGCTGGCCGAGACAGCGCCAGCAGC 120
DB 214 GCCCAGTGGCCCCCAGGACCTTGTGTCAGAGCGGCTGGCCGAGACAGCGCCAGCAGC 273
QY 121 TGTGGCCCGTGTCCACCGCGCACTTACAGGAGTTTGGAACTACTTGGAGCGCTGCCGC 180
DB 274 TGTGGCCCGTGTCCACCGCGCACTTACAGGAGTTTGGAACTACTTGGAGCGCTGCCGC 333
QY 181 TATCGCAACGCTCTCTGCGGGGAGCGTGAAGAGAGAGAGCGGCTTGCACAGCCAC 240
DB 334 TATCGCAACGCTCTCTGCGGGGAGCGTGAAGAGAGAGAGCGGCTTGCACAGCCAC 393
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DB 934 CGGAGCGCTCCGTGAGCGCTTCTCTCTCTGTCAC 966

RESULT 7
AX055373 1114 bp DNA linear PAT 13-JAN-2001
LOCUS Sequence 3 from Patent WO0073452.
ACCESSION AX055373
VERSION AX055373.1 GI:12228659
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Ashkenazi, A., Baker, K.P., Chan, B., Goddard, A., Godowski, P.J.,
Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L.,
Tumas, D., Watanabe, C.K. and Wood, W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 3 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
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BASE COUNT 188 a 379 c 356 g 191 t
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Query Match 100.0%; Score 813; DB 6; Length 1114;
Best Local Similarity 100.0%; Pred. No. 6, 6e-125;
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DB 188 GTGGCAGAAACACCCACTTACCTTGGCGGAGCAGAGAGAGAGAGGAGCGGCTGTGTGC 247

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Source	Organism	Title	Reference Authors	Journal	Medline	PubMed	Authors	Features	Source
Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
1 (bases 1 to 1114)									
Pitli, R.M., Marsters, S.A., Lawrence, D.A., Roy, M., Kischkel, F.C., Dowd, P., Huang, A., Donahue, C.J., Sherwood, S.W., Baldwin, D.T., Godowski, P.J., Wood, W.I., Gurney, A.L., Hillan, K.J., Cohen, R.L., Goddard, A.D., Botstein, D. and Ashkenazi, A.									
Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer									
Nature 396 (6712), 699-703 (1998)									
99087326									
2 (bases 1 to 1114)									
Pitli, R.M., Marsters, S.A., Lawrence, D.A., Roy, M., Kischkel, F.C., Dowd, P., Huang, A., Donahue, C.J., Sherwood, S.W., Baldwin, D.T., Godowski, P.J., Wood, W.I., Gurney, A.L., Hillan, K.J., Cohen, R.L., Goddard, A.D., Botstein, D. and Ashkenazi, A.									
Direct Submission									
Submitted (04-NOV-1998)									
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LOCUS BC017065

DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member 6b, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds.

ACCESSION BC017065

VERSION BC017065.1 GI:16877637

KEYWORDS MGC.

ORGANISM Homo sapiens.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1125)

AUTHORS Strausberg, R.

JOURNAL Direct Submission

Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgaps-rc@mail.nih.gov](mailto:cgaps-rc@mail.nih.gov)

Tissue Procurement: DCTD/DTF/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) [mc@paxil.stanford.edu](mailto:mc@paxil.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 22 Row: d Column: 23  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 14790166.

## FEATURES

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Query Match 100.0%; Score 813; DB 9; Length 1125;  
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ACCESSION AX017828  
VERSION AX017828.1 GI:10042431  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1168)  
AUTHORS Kroeger, B.  
TITLES Receptor, from the superfamily of tnt-receptors from the human lung  
JOURNAL Patent: WO 9946376-A 1 16-SEP-1999;  
BASIS AG (DE); KROEGER BURKHARD (DE)  
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VERSION AR171895.1 GI:17910845  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1347)  
AUTHORS Triboley, C.  
TITLE Polynucleotide encoding TNF1  
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VERSION AF217793.1 GI:6969260  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 1428)  
AUTHORS Bal, C., Connolly, B., Metzger, M.L., Hilliard, C.A., Liu, X.,  
Sanding, V., Soderman, A., Galloway, S.M., Liu, Q., Austin, C.P. and  
Caekey, C.T.  
TITLE Overexpression of M68/DCR3 in human gastrointestinal tract tumors  
independent of gene amplification and its location in a four-gene  
cluster  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)  
MEDLINE 20122600  
PUBMED 10655513  
REFERENCE 2 (bases 1 to 1428)  
AUTHORS Bal, C.  
TITLE Direct Submission  
JOURNAL Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories,



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Db	1122	CAGCGCTGTGTCAGGCCCTCGAGCCCGGAGGCGTGGGTTCGCACACCAAGGCGGCG	1181		
Qy	661	CGCGCGGCTTTGCAGCTGAAGCTGCGTGGCGGCTCAGCGAGCTCTCTGGGGCGCAGGAC	720		



VIRDAQFRVARTMPAPAPATAPSVAGEDAVSEAKSPGPFSTRKAKSLDLHVS  
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BASE COUNT 963 a 1581 c 1529 g 872 t  
ORIGIN

Query Match 100.0%; Score 813; DB 9; Length 4945;  
Best Local Similarity 100.0%; Pred. No. 4.9e-125;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGACAGAAACACCACTACCCCTGGCGGAGACAGAGAGAGGAGCGCTGTGTGC 60  
DB GTGACAGAAACACCACTACCCCTGGCGGAGACAGAGAGAGGAGCGCTGTGTGC 4054  
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QY 181 TACTGCAACGCTCTGTGCGGGGAGCGTAGAGAGAGGACGCGCTTGCCAGCGCCACCAC 240  
DB 4175 TACTGCAACGCTCTGTGCGGGGAGCGTAGAGAGAGGACGCGCTTGCCAGCGCCACCAC 4224  
QY 241 AACCGTCCGTGCGCTGCCGACCGGCTTCTTGCGCAGCGCTGTTCTGCTTGAGACAC 300  
DB 4235 AACCGTCCGTGCGCTGCCGACCGGCTTCTTGCGCAGCGCTGTTCTGCTTGAGACAC 4294  
QY 301 GCATGCTGTCACTGTGTGCGGGGTATTTGCCCGGGACACCCCGACGAGAACACGACG 360  
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QY 721 GGGGCGGTGTGAGGCGCTGCTGAGGCGCTGCGGCGTGGCAGAGTCCCGGGGCTGGAG 780  
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DB 4775 CGGAGCGTCCGTGAGCGCTTCTCTCTGTGAC 4807

# RESULT 15

BC034349

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BC034349 1150 bp mRNA linear PRI 08-JUL-2002  
Homo sapiens, tumor necrosis factor receptor superfamily, member  
6b, decoy, clone MGC:21079 IMAGE:4752507, mRNA, complete cds.  
BC034349  
BC034349.1 GI:21706464  
MGC.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 1150)  
Strausberg, R.  
Direct Submission  
Submitted (02-JUL-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

## REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
Series: IRK Plate: 28 Row: 0 Column: 15  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 14790166.  
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## FEATURES

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## CDS

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BASE COUNT 222 a 382 c 348 g 198 t

ORIGIN

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Best Local Similarity 99.9%; Pred. No. 1.2e-124;  
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Db 256 GCCAGTGCCTCCAGGACACTTTGTGCAGGGCCGTGCGCCGAGACAGGCCACACGACG 315  
QY 121 TGTGGCCCGTGTCCACCGCCCACTACACGAGTTCTTGGAACTACCTGGAGCGCTGCCGC 180  
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QY 241 AACCGTGCCTGCCGCTGCCGACCGGCTTCTTGCAGCACTGTTCTTGGAGCAC 300  
Db 436 AACCGTGCCTGCCGCTGCCGACCGGCTTCTTGCAGCACTGTTCTTGGAGCAC 495  
QY 301 GCATCGTGTCCACCTGCTGCGGGGTGATTGCCCGGGACACCCCGAGCAAGACGCGAG 360  
Db 496 GCATCGTGTCCACCTGCTGCGGGGTGATTGCCCGGGACACCCCGAGCAAGACGCGAG 555  
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Db 556 TGCAGCGCTGCCCGCCAGGACACCTTCTCAGCCAGCAGAGCTCCAGCTCAGAGCAGTGCCAG 615  
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QY 781 CGGAGCGTCCGTGAGCGCTTCCCTCCCTGTGCAC 813  
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 12:53:01 ; Search time 230 Seconds

(without alignments)  
7960.324 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813

Sequence: 1 ggcgcagaacaccacaccta.....agcgtctctccctgcac 813

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	813	100.0	813	20	AAZ25377
2	813	100.0	813	21	AAZ75999
3	813	100.0	813	21	AAZ88730
4	813	100.0	813	21	AAZ51077
5	813	100.0	813	22	AAZ07380
6	813	100.0	813	24	AAZ27868
7	813	100.0	900	21	AAZ25375
8	813	100.0	900	21	AAZ53208
9	813	100.0	900	21	AAZ51075

10	813	100.0	903	20	AAZ22300	Orphan receptor (H
11	813	100.0	1055	22	AAZ62705	Human NTR3 nucleot
12	813	100.0	1066	21	AAZ53802	M68 TNF receptor r
13	813	100.0	1077	19	AAV39085	Human tumour necro
14	813	100.0	1077	21	AAZ37772	Human tumour necro
15	813	100.0	1077	24	AAZ33281	Human tumour necro
16	813	100.0	1114	21	AAZ32744	Human DCR3 polypep
17	813	100.0	1114	21	AAZ58367	Human PRO212 nucle
18	813	100.0	1114	21	AAZ58581	Human PRO212 prote
19	813	100.0	1114	21	AAZ75337	Human PRO212 CDNA
20	813	100.0	1114	22	AAZ84421	Human PRO212 poly
21	813	100.0	1164	19	AAZ91462	Human PRO212 CDNA
22	813	100.0	1164	22	AAZ07654	Nucleotide sequenc
23	813	100.0	1168	20	AAZ09998	Human lung TNF-rec
24	813	100.0	1179	22	AAZ33171	Human colon cancer
25	813	100.0	1205	20	AAZ07226	Human tumour necro
26	813	100.0	1347	20	AAZ63764	Human soluble TNF
27	813	100.0	1428	21	AAZ53801	M68 TNF receptor r
28	813	100.0	1462	20	AAZ76052	Mammalian tumour n
29	811.4	99.8	825	20	AAZ25378	Human mFLINT #2 nu
30	811.4	99.8	825	21	AAZ51078	Human mature FLINT
31	811.4	99.8	936	20	AAZ25376	Human FLINT #2 nuc
32	809.8	99.6	936	21	AAZ88731	Human FAS ligand i
33	809.8	99.6	936	21	AAZ51076	Human FLINT coding
34	809.8	99.6	936	22	AAZ07385	Human fas ligand i
35	809.8	99.6	936	22	AAZ89920	Nucleotide sequenc
36	809.8	99.6	936	22	AAZ84738	Nucleotide sequenc
37	809.8	99.6	936	22	AAZ84739	Nucleotide sequenc
38	809.8	99.6	936	22	AAZ7696	Human FLINT native
39	809.8	99.6	936	24	AAZ27869	Human FLINT analog
40	809.8	99.6	1137	21	AAZ92404	CDNA encoding huma
41	798.6	98.2	1224	24	ABO55057	Human ovarian anti
42	728.2	89.6	900	21	AAZ53209	Monkey Fas ligand
43	647	79.6	767	20	AAZ23419	Human APO6 DNA. H
44	644.2	79.2	899	20	AAZ89503	DNA encoding a hum
45	533.4	65.6	1859	21	AAZ63765	Human soluble TNF

#### ALIGNMENTS

RESULT 1	AAZ25377	standard; cDNA; 813 BP.
XX	AAZ25377:	
AC	17-DEC-1999	(first entry)
XX		
DT	Human mFLINT #1 nucleotide sequence.	
XX		
DE	Human, FLINT, mFLINT, OPB3; tumour necrosis factor receptor; FasL; apoptosis; inflammation; cancer; diabetes; acute liver failure; sepsis; hepatitis; ischaemia-associated injury; hypercoagulation; reperfusion-associated injury; aplastic anaemia; differentiation; growth; myelodysplastic syndrome; pancytopenic condition; myocardial ischaemia; ss.	
KW	Homo sapiens.	
XX		
OS	WO9950413-A2.	
XX		
PN	07-OCT-1999.	
XX		
PD	30-MAR-1999;	99WO-US06797.
XX		
PF	30-MAR-1998;	98US-0079856.
XX		
PR	20-MAY-1998;	98US-0086074.
XX		
PR	09-SEP-1998;	98US-0099643.
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PR	17-DEC-1998;	98US-0112577.
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PR	18-DEC-1998;	98US-0112703.
XX		
PR	18-DEC-1998;	98US-0112933.
XX		
PR	22-DEC-1998;	98US-0113407.

XX (ELIL ) LILLY & CO ELI.  
PI Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;  
PI Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;  
PI Song HY, Wang J, Wu X, Zuckerman SH;  
XX WPI; 1999-591319/50.  
DR P-PSDB; AA242184.  
XX  
PT Use of mature FLINT for treating acute liver failure, inflammation,  
PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic  
PT and proinflammatory activity  
XX  
PS Claim 29; Fig 3; 99pp; English.  
XX  
CC The present invention describes therapeutic applications of mature FLINT  
CC (mFLINT) for use in the treatment of acute liver failure. Mature FLINT  
CC (mFLINT), which is a member of the tumor necrosis factor receptor  
CC superfamily, is used for treating acute liver failure, inflammation of  
CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated  
CC with inflammation, hepatitis, abnormal apoptosis, an ischemia-associated  
CC injury or disorder such as hypercoagulation (including use with  
CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury  
CC or disorder, type I diabetes, cancer, cell damage or damage to an  
CC innocent bystander tissue that is induced by a chemotherapeutic agent or  
CC therapeutic irradiation, treating hematopoietic progenitor cells that  
CC have been exposed to therapeutic radiation or chemotherapy, aplastic  
CC anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is  
CC also used for promoting the growth or differentiation of a hematopoietic  
CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte  
CC resulting from abnormal myocardial ischemia. The present sequence  
CC encodes human mFLINT.  
XX  
SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;  
Query Match 100.0%; Score 813; DB 20; Length 813;  
Best Local Similarity 100.0%; Pred. No. 5.1e-145;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 GTGGCAGAAACACCACTACCTGGCGGACGAGACAGGGAGCGGTGGTGC 60  
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QY 121 TGTGGCGCGTGTCCACGGCGCCTACACGACGTTCTGGAACTACCTGGAGCGCTGCCGC 180  
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DB 181 TACTGCAAGCTCTCTGCGGGAGCGTGGAGGAGGACGCGGCTTGCACGCGCCAC 240  
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DB 241 AACCGTGGCTTGGCGTCCCGACCGGCTTCTTCCGACGCTGTTCTGCTTGGAGCAC 300  
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DB 361 TGCAGCGGTGCCCCCAGGACCTTCTCAGCCAGACGAGTCCAGCTCAGAGAGTCCAG 420  
QY 421 CCCACCGCAACTGCACGGCGCTGGCGCTCCAAATGTGCAGGCTCTTCTCCCAT 480  
DB 421 CCCACCGCAACTGCACGGCGCTGGCGCTCCAAATGTGCAGGCTCTTCTCCCAT 480  
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DB 481 GACACCTGTGCACAGCTGCACTGGCTTCCCTCCAGCAGGATACAGAGCTGAG 540  
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DB 541 GAGTGTGAGCGTGGCGTCAATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600  
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DB 601 CAGCGGCTCTGAGGCGCTTCGAGGCGCCCGAGGGGTGGGTCCGACACCAAGGGCGGGC 660  
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DB 661 CCGCGGCGCTTCGAGCTGAAGCTGCGTGGCGGCTCACGAGCTCTCGGGGCGCAGGAC 720  
QY 721 GGGGCGCTCTGCTGGCGGCTGCTGCAGGCGCTGCGGCTGGCCAGGATGCCCGGCTGGAG 780  
DB 721 GGGGCGCTCTGCTGGCGGCTGCTGCAGGCGCTGCGGCTGGCCAGGATGCCCGGCTGGAG 780  
QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813  
DB 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813  
RESULT 2  
AAA75999  
ID AAA75999 standard; DNA; 813 BP.  
XX  
AC AAA75999;  
XX  
DT 19-FEB-2001 (first entry)  
XX  
DE DNA encoding a mature human FAS Ligand Inhibitory Protein (FLINT).  
XX  
KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;  
KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;  
KW acute respiratory distress syndrome; ulcerative colitis;  
KW chronic obstructive pulmonary disease; Crohn's disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200058465-A2.  
XX  
PD 05-OCT-2000.  
XX  
PF 20-MAR-2000; 2000WO-US06417.  
XX  
PR 30-MAR-1999; 99US-0126839.  
PR 21-JUN-1999; 99US-0140077.  
PR 21-JUN-1999; 99US-0140156.  
PR 20-OCT-1999; 99US-0160566.  
PR 18-FEB-2000; 2000US-0183398.  
XX  
PA (ELIL ) LILLY & CO ELI.  
XX  
PI Becker GW, Cohen FU, Gonzalez-dewhitt PA, Hale JE, Micanovic R;  
PI Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;  
PI Wroblewski VJ;  
XX  
DR WPI; 2000-656167/63.  
DR P-PSDB; AAB19334.  
XX  
PT FAS Ligand Inhibitory Protein analogs useful for treating abnormal  
PT apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,  
PT chronic obstructive pulmonary disease ulcerative colitis or Crohn's  
PT disease  
XX  
PS Claim 37; Page 113; 114pp; English.  
XX  
CC The present sequence encodes a mature human FAS Ligand Inhibitory  
CC protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor  
CC proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature  
CC FLINT protein is modified to produce analogues, which have greater

CC potency, longer in vivo half-lives, decreased aggregation, decreased  
 CC absorption onto surfaces, increased solubility and improved ease of  
 CC formulation. The FLINT analogue is useful for treating a patient  
 CC suffering from disease or condition relating to abnormal apoptosis such  
 CC as acute lung injury, acute respiratory distress syndrome, pulmonary  
 CC fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or  
 CC Crohn's disease.

XX Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match 100.0%; Score 813; DB 21; Length 813;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-145;

Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAAAACACCCACTACCTCCCTGGCGGAGACAGAGACAGGGAGCGGCTGTGTC 60  
 DB 1 GTGGCAAAACACCCACTACCTCCCTGGCGGAGACAGAGACAGGGAGCGGCTGTGTC 60  
 QY 61 GCCCAGTGCCTCCCGGAGCACTTTGTGACAGCGGCGCTGCGCGAGACAGCCCGACGAGC 120  
 DB 61 GCCCAGTGCCTCCCGGAGCACTTTGTGACAGCGGCGCTGCGCGAGACAGCCCGACGAGC 120  
 QY 121 TGTGGCCCGGTGTCCACCGCGCACTACACGAGTTCTGGAACCTGAGCGCTGCGC 180  
 DB 121 TGTGGCCCGGTGTCCACCGCGCACTACACGAGTTCTGGAACCTGAGCGCTGCGC 180  
 QY 181 TACTGCAACGCTCTGTGGGGGAGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 DB 181 TACTGCAACGCTCTGTGGGGGAGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 QY 241 AACCGTGCCTGCGCGTGCACGAGCGCTTCTTGCAGCAGCGTGTGTTCTGTTGAGACAC 300  
 DB 241 AACCGTGCCTGCGCGTGCACGAGCGCTTCTTGCAGCAGCGTGTGTTCTGTTGAGACAC 300  
 QY 301 GCATCGTGTCCACTGTGTGCGCGGTGATTTGCCCGGACACCCCGACGAGACGACGAC 360  
 DB 301 GCATCGTGTCCACTGTGTGCGCGGTGATTTGCCCGGACACCCCGACGAGACGACGAC 360  
 QY 361 TGCAGCGCGTGCCTGCGGAGCACTTTCAGCCAGCAGCTTCAGAGAGAGAGAGAGAGAG 420  
 DB 361 TGCAGCGCGTGCCTGCGGAGCACTTTCAGCCAGCAGCTTCAGAGAGAGAGAGAGAGAG 420  
 QY 421 CCCCAACGCACTGACAGCGGCTGAGCGCTGAGCGCTTCAATGTGACAGCGCTTCTCCCAT 480  
 DB 421 CCCCAACGCACTGACAGCGGCTGAGCGCTGAGCGCTTCAATGTGACAGCGCTTCTCCCAT 480  
 QY 481 GACACCTGTGACACGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 540  
 DB 481 GACACCTGTGACACGACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 540  
 QY 541 GAGTGTAGGCTGCGCTGATGATTTGTGCTTCCAGAGACATCTTCATCAAGAGCTG 600  
 DB 541 GAGTGTAGGCTGCGCTGATGATTTGTGCTTCCAGAGACATCTTCATCAAGAGCTG 600  
 QY 601 CAGCGGCTGTGACAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 660  
 DB 601 CAGCGGCTGTGACAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 660  
 QY 661 CGCGGAGCTTTGACGCTGAAAGCTGCTGCGGAGCTCAAGAGCTTCTGAGGAGCGAGAC 720  
 DB 661 CGCGGAGCTTTGACGCTGAAAGCTGCTGCGGAGCTCAAGAGCTTCTGAGGAGCGAGAC 720  
 QY 721 GGGGCGTGTGTGTGCGGCTGTGACAGCGCTGTGCGGTGCGAGAGATGCCGGGCTGAG 780  
 DB 721 GGGGCGTGTGTGTGCGGCTGTGACAGCGCTGTGCGGTGCGAGAGATGCCGGGCTGAG 780  
 QY 781 CGAGCGCTGTGAGCGCTTCTCTCTGTGAC 813  
 DB 781 CGAGCGCTGTGAGCGCTTCTCTCTGTGAC 813

RESULT 3  
 AAA88730

ID AAA88730 standard; cDNA; 813 BP.  
 XX  
 AC AAA88730;  
 XX  
 DT 05-FEB-2001 (first entry)  
 XX  
 DE Human FAS ligand inhibitor protein FLINT cDNA.  
 XX  
 KW FLINT; FAS ligand inhibitor protein; human; protease resistant;  
 KW acute lung injury; acute respiratory distress syndrome;  
 KW chronic obstructive pulmonary disease; pulmonary fibrosis;  
 KW ulcerative colitis; therapy; organ transplantation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200058466-A2.  
 PD 05-OCT-2000.  
 XX  
 PF 20-MAR-2000; 2000MO-US06418.  
 XX  
 PR 30-MAR-1999; 99US-0126839.  
 PR 21-JUN-1999; 99US-0140073.  
 PR 04-AUG-1999; 99US-0147071.  
 PR 20-OCT-1999; 99US-0160524.  
 PR 21-OCT-1999; 99US-0160669.  
 PR 20-DEC-1999; 99US-0172744.  
 PR 26-JUN-2000; 2000US-0178184.  
 XX  
 PA (ELIL) LILLY & CO ELI.  
 XX  
 PI Micanovic R, Rathnachalam R, Wichter DR;  
 XX  
 DR WPI; 2000-664925/64.  
 XX  
 PT P-PSDB; AAB19705.  
 XX  
 PT Novel protease resistant FAS ligand inhibitory protein analogues  
 PT resistant to in vivo or in vitro proteolysis at amino acid position 218  
 PT of the mature protein, useful for treating autoimmune diseases -  
 XX  
 PS disclosure; Page 95; 100pp; English.  
 XX  
 CC The present sequence is that of cDNA coding for human FAS ligand  
 CC inhibitory protein FLINT mature protein (see AAB19705). FLINT is a  
 CC tumour necrosis factor receptor homologue that binds FAS ligand,  
 CC preventing its interaction with FAS. This interaction is implicated  
 CC in runaway apoptosis and inflammatory disease. FLINT also binds to  
 CC LIGHT, a membrane-bound ligand, which may play a role in immune  
 CC modulation and apoptosis. The invention relates to novel FLINT  
 CC analogues (see also AAB19706-09) that are resistant to proteolysis  
 CC by trypsin-like proteases between positions 218 and 219 of the  
 CC FLINT mature protein sequence. Nucleic acids, vectors and  
 CC transformed host cells for recombinant production of the analogues  
 CC are claimed. FLINT cDNA is used as a template for introducing the  
 CC required point mutations e.g. via PCR mutagenesis. The protease  
 CC resistant FLINT analogues are used to prevent or treat acute lung  
 CC injury, acute respiratory stress syndrome, ulcerative colitis,  
 CC chronic obstructive pulmonary disease, pulmonary fibrosis, to  
 CC inhibit T lymphocyte activation, and to facilitate organ  
 CC preservation for transplantation (claimed).  
 XX  
 SO Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match 100.0%; Score 813; DB 21; Length 813;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-145;  
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAAAACACCCACTACCTCCCTGGCGGAGACAGAGACAGGGAGCGGCTGTGTC 60  
 DB 1 GTGGCAAAACACCCACTACCTCCCTGGCGGAGACAGAGACAGGGAGCGGCTGTGTC 60  
 QY 61 GCCCAGTGCCTCCCGGAGCACTTTGTGACAGCGGCGCTGCGCGAGACAGCCCGACGAGC 120



Db 421 CCCACCGCACTGCACGCGCCCTGGCCCTCAATGTGCCAGGCTCTTCTCCCAT 480  
 Qy 481 GACACCCCTGTGCACAGCTGACTGCTTCCCTCCAGCACAGGATACAGAGCTGAG 540  
 Db 481 GACACCCCTGTGCACAGCTGACTGCTTCCCTCCAGCACAGGATACAGAGCTGAG 540  
 Qy 541 GAGTGTAGGCGTGCCTGATGACTGCTTGTGCTTCCAGACATCTCATCAGAGGCTG 600  
 Db 541 GAGTGTAGGCGTGCCTGATGACTGCTTGTGCTTCCAGACATCTCATCAGAGGCTG 600  
 Qy 601 CAGCGCTGCTGCACGCGCTTCGAGGCCCGAGAGGCTGGGCTCCGACACCAAGGCGGCGC 660  
 Db 601 CAGCGCTGCTGCACGCGCTTCGAGGCCCGAGAGGCTGGGCTCCGACACCAAGGCGGCGC 660  
 Qy 661 CGCGCGCTGTGACGCTGAACTGCGTGGGCGGCTCACGAGGCTCTGGGGGGCCAGGAC 720  
 Db 661 CGCGCGCTGTGACGCTGAACTGCGTGGGCGGCTCACGAGGCTCTGGGGGGCCAGGAC 720  
 Qy 721 GGGGCGCTGTGCTGCTGCGGCTGCTGCAGGCGCTGCGCTGGCAGAGATGCCGCGGCTGGAG 780  
 Db 721 GGGGCGCTGTGCTGCTGCGGCTGCTGCAGGCGCTGCGCTGGCAGAGATGCCGCGGCTGGAG 780  
 Qy 781 CGGAGCGTCCGTGAGCGCTTCTCTCTCTGTCAC 813  
 Db 781 CGGAGCGTCCGTGAGCGCTTCTCTCTCTGTCAC 813

## RESULT 5

AAD07380 standard; cDNA; 813 BP.  
 AAD07380;

04-AUG-2001 (first entry)  
 Human mature fas ligand inhibitory protein (FLINT) cDNA.

Human mature fas ligand inhibitory protein (FLINT) cDNA.  
 Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI; TNFR; tumor necrosis factor receptor protein; ulcerative colitis; ARDS; acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy; rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis; fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis; chronic renal failure; graft-vs-host disease; cutaneous inflammation; vascular leak syndrome; Helicobacter pylori infection; atherosclerosis; insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease; Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis; Down's syndrome; multiple sclerosis; cytostatic; nootropic; neuroprotective; vasotropic; ss.

Homo sapiens.

Key Location/Qualifiers  
 CDS 1..813

/product= a  
 (FLINT)  
 /note= "Human mature fas ligand inhibitory protein  
 /partial

MO200142463-A1.

14-JUN-2001.

29-NOV-2000; 2000MO-US30166.

07-DEC-1999; 99US-0169367.

07-DEC-1999; 99US-0169381.

23-MAR-2000; 2000US-0191430.

(ELIL) LILLY & CO ELI.

PI Lu J, Wlitcher DR;  
 XX WPI: 2001-381684/40.  
 DR P-PDB; AA03567.  
 XX  
 PT New FLINT polypeptide for treating and/or preventing acute lung injury,  
 PT acute respiratory distress syndrome, ulcerative colitis, and  
 PT graft-versus-host disease, comprises O-linked or N-linked  
 PT oligosaccharides -  
 XX  
 PS Example 1; Page 53; 60pp; English.

The present sequence is human mature fas ligand inhibitory protein  
 (FLINT) cDNA. FLINT, a homologue of tumor necrosis factor receptor  
 protein (TNFR), binds fas ligand (FasL) and thereby preventing the  
 interaction of FasL with Fas. FLINT comprising O-linked or N-linked  
 oligosaccharides is useful for preventing or treating acute lung injury  
 (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,  
 chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),  
 CC to facilitate organ preservation for transplantation and to inhibit T  
 CC lymphocyte activation. FLINT is useful for treating and/or preventing  
 CC diseases such as rheumatoid arthritis, fibroproliferative lung disease,  
 CC fibrotic lung disease, acute lung injury, human immunodeficiency virus  
 CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-  
 CC host disease, cutaneous inflammation, vascular leak syndrome,  
 CC Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent  
 CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,  
 CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as  
 CC psoriasis, Down's syndrome, and multiple sclerosis.

Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;

Query Match 100.0%; Score 813; DB 22; Length 813;

Best Local Similarity 100.0%; Pred. No. 5, 1e-145; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGACAGACAGAGGAGCGGCTGTGTC 60  
 Db 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGACAGACAGAGGAGCGGCTGTGTC 60  
 Qy 61 GCCAGTGTCCCGGAGGACCTTTGTGACGCGCGCTGCGCGAGACAGCCCGACGAGC 120  
 Db 61 GCCAGTGTCCCGGAGGACCTTTGTGACGCGCGCTGCGCGAGACAGCCCGACGAGC 120  
 Qy 121 TGTGCGCCGTGTCCACCGCGGCTACACGAGTTCTGGAATCACTTGAGCGCTGCGC 180  
 Db 121 TGTGCGCCGTGTCCACCGCGGCTACACGAGTTCTGGAATCACTTGAGCGCTGCGC 180  
 Qy 181 TACTGCAACGCTCTCTGCGGAGAGCGTGAAGAGGACAGGCGTTGCAAGCCACCCAC 240  
 Db 181 TACTGCAACGCTCTCTGCGGAGAGCGTGAAGAGGACAGGCGTTGCAAGCCACCCAC 240  
 Qy 241 AACGTCCTGCGGCTGCGACCGGCTTCTTCCGACGCTGGTTTCTGTTGAGACAC 300  
 Db 241 AACGTCCTGCGGCTGCGACCGGCTTCTTCCGACGCTGGTTTCTGTTGAGACAC 300  
 Qy 301 GCATGCTGTCACCTGTGTCGCGGCTGATTTGCCCGGACCCCGACGACACCCAG 360  
 Db 301 GCATGCTGTCACCTGTGTCGCGGCTGATTTGCCCGGACCCCGACGACACCCAG 360  
 Qy 361 TGCCAGCGTGCCTGCGGAGGACCTTCTGACGACGAGCTCCAGCTAGAGAGTGCGAG 420  
 Db 361 TGCCAGCGTGCCTGCGGAGGACCTTCTGACGACGAGCTCCAGCTAGAGAGTGCGAG 420  
 Qy 421 CCCACCGCAACTGCACGCGCTGGGCTGGGCTCCATGTGCGAGGCTTCTTCCCAT 480  
 Db 421 CCCACCGCAACTGCACGCGCTGGGCTGGGCTCCATGTGCGAGGCTTCTTCCCAT 480  
 Qy 481 GACACCTGTGCACAGCTGACTGCTTCCCTTCAGCACAGGATACAGAGCTGAG 540  
 Db 481 GACACCTGTGCACAGCTGACTGCTTCCCTTCAGCACAGGATACAGAGCTGAG 540  
 Qy 541 GAGTGTAGGCGTGCCTGATGACTTGTGCTTCCAGACATCTCATCAGAGGCTG 600

|||||  
Db 541 GAGTGTGAGCGTCCGTCATCGACTTTGTGCTTTCAGAGACAATCCATCAAGAGCTG 600  
QY 601 CAGCGGCTGTGACAGGCTTCGAGGCCCCGAGGCTGGGGTCCGACACCAAGGGCGGC 660  
Db 601 CAGCGGCTGTGACAGGCTTCGAGGCCCCGAGGCTGGGGTCCGACACCAAGGGCGGC 660  
QY 661 CGCGCGCTTTGACGCTGAAGCTGCGTGGCGGCTACCGAGCTCTGGGGGCGCAGGAC 720  
Db 661 CGCGCGCTTTGACGCTGAAGCTGCGTGGCGGCTACCGAGCTCTGGGGGCGCAGGAC 720  
QY 721 GCGGCGCTGTGCTGCGGCTGTCGAGGCGCTGCGGCTGCCAGGATGCCCGGCTGGAG 780  
Db 721 GCGGCGCTGTGCTGCGGCTGTCGAGGCGCTGCGGCTGCCAGGATGCCCGGCTGGAG 780  
QY 781 CGGAGCGTCCGTCAGCGCTTCTCCCTGTGCAC 813  
Db 781 CGGAGCGTCCGTCAGCGCTTCTCCCTGTGCAC 813  
RESULT 6  
AAD27868  
ID AAD27868 standard; DNA; 813 BP.  
XX AC AAD27868;  
XX 01-JUL-2002 (first entry)  
XX Human mature FLINT DNA.  
KW FLINT; FAS ligand inhibitory protein; pulmonary; lung; apoptosis;  
KW organ failure; liver; kidney; pancreas; inflammatory disease;  
KW neutrophil; sepsis; acute respiratory distress syndrome;  
KW acute lung injury; systemic inflammatory response syndrome; SIRS;  
KW multiple organ dysfunction; MODS; human; gene; ds.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 1..813  
FT CDS /tag= a  
FT /product= "Mature FLINT protein"  
FT /note= "Does not include start and stop codons"  
FT /partial  
XX WO200209668-A2.  
PN  
XX  
XX 07-FEB-2002.  
XX  
XX 20-JUL-2001; 2001WO-US21105.  
XX  
XX 02-AUG-2000; 2000US-222476P.  
XX  
XX (ELIL ) LILLY & CO ELI.  
XX  
XX Micanovic R, Witcher DR;  
XX  
XX WPI; 2002-206149/26.  
XX P-PSDB; AAE14578.  
XX  
XX Administering FLINT (FAS ligand inhibitory protein) or FLINT analog,  
PT useful for treating e.g. sepsis or respiratory distress syndrome,  
PT involves pulmonary administration of a therapeutic amount of the FLINT  
PT or FLINT analog -  
XX  
XX Disclosure; Page 30; 35pp; English.  
XX  
XX The invention relates to a new method of administering FLINT  
CC (FAS ligand inhibitory protein) or FLINT analog that involves pulmonary  
CC administration of a therapeutic amount of the FLINT or FLINT analog.  
CC The method enables systemic absorption of FLINT through lungs and  
CC significantly reduces or eliminates the need for administering FLINT by  
CC injection or other routes of administration. The method is useful in

CC treating disorders related to enhanced apoptosis (e.g. organ failure  
CC in liver, kidneys and pancreas) and inflammatory diseases associated with  
CC neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,  
CC acute lung injury, systemic inflammatory response syndrome (SIRS) and  
CC multiple organ dysfunction (MODS)). The method minimises the pain  
CC and discomfort of injection methods. The present sequence is human  
CC mature FLINT DNA.  
XX  
SQ Sequence 813 BP; 122 A; 298 C; 267 G; 126 T; 0 other;  
Query Match 100.0%; Score 813; DB 24; Length 813;  
Best Local Similarity 100.0%; Pred. No. 5.1e-145;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGCAGAAACACCCACCTTACCCCTGGCGGACGACAGACAGAGGAGCGGTGGTGTGC 60  
Db 1 GTGGCAGAAACACCCACCTTACCCCTGGCGGACGACAGACAGAGGAGCGGTGGTGTGC 60  
QY 61 GCCAGTGGCCCCCAGGACACCTTTGTGACGCGCGCTGCGCGGACAGCCCCAGACG 120  
Db 61 GCCAGTGGCCCCCAGGACACCTTTGTGACGCGCGCTGCGCGGACAGCCCCAGACG 120  
QY 121 TGTGGCCCGTGTCCACCGGCCACTACACGCACTTCTGAACTTACCTGGAGCGCTGCCG 180  
Db 121 TGTGGCCCGTGTCCACCGGCCACTACACGCACTTCTGAACTTACCTGGAGCGCTGCCG 180  
QY 181 TACTGCAACGTCCTCTGCGGGGAGCGTAGGAGGAGGACACGCGCTTGCACGCCAC 240  
Db 181 TACTGCAACGTCCTCTGCGGGGAGCGTAGGAGGAGGACACGCGCTTGCACGCCAC 240  
QY 241 AACCGTGGCTGGCGTGGCGCACCGGCTTCTTCGCGCACGCTGTTCTGCTTGGAGCAC 300  
Db 241 AACCGTGGCTGGCGTGGCGCACCGGCTTCTTCGCGCACGCTGTTCTGCTTGGAGCAC 300  
QY 301 GCATCGTGTCCACCTGGTGGCGCGTGATTGCCCGGGGACCCCGGACAGCAACAGCAG 360  
Db 301 GCATCGTGTCCACCTGGTGGCGCGTGATTGCCCGGGGACCCCGGACAGCAACAGCAG 360  
QY 361 TGCACGCGTGGCCCCCAGGACACCTTCTCAGCGAGAGCTTCCAGCTCAGAGAGTGCAC 420  
Db 361 TGCACGCGTGGCCCCCAGGACACCTTCTCAGCGAGAGCTTCCAGCTCAGAGAGTGCAC 420  
QY 421 CCCACCGCAACTGCACGCGCTGGCGCTGGCGCTCAATGTGCGAGGCTTCTCCCTCCCAT 480  
Db 421 CCCACCGCAACTGCACGCGCTGGCGCTGGCGCTCAATGTGCGAGGCTTCTCCCTCCCAT 480  
QY 481 GACACCTGTGCACACGAGCTGCACTGGCTTCCCCCTCAGCACACAGGCTTACAGAGCTGAG 540  
Db 481 GACACCTGTGCACACGAGCTGCACTGGCTTCCCCCTCAGCACACAGGCTTACAGAGCTGAG 540  
QY 541 GAGTGTGAGCGTGCCTCATTCGACTTTTGGCTTTCAGGACATCTCCATCAAGAGGCTG 600  
Db 541 GAGTGTGAGCGTGCCTCATTCGACTTTTGGCTTTCAGGACATCTCCATCAAGAGGCTG 600  
QY 601 CAGCGGCTGTGACGCGCTTCGAGGCCCCGAGGCTGGGGTCCGACACCAAGGGCGGC 660  
Db 601 CAGCGGCTGTGACGCGCTTCGAGGCCCCGAGGCTGGGGTCCGACACCAAGGGCGGC 660  
QY 661 CGCGCGCTTTGACGCTGAAGCTGCGTGGCGGCTCAGCGAGCTCTGGGGGCGCAGGAC 720  
Db 661 CGCGCGCTTTGACGCTGAAGCTGCGTGGCGGCTCAGCGAGCTCTGGGGGCGCAGGAC 720  
QY 721 GCGGCGCTGTGCTGCGGCTGTCGAGGCGCTGCGGCTGCCAGGATGCCCGGCTGGAG 780  
Db 721 GCGGCGCTGTGCTGCGGCTGTCGAGGCGCTGCGGCTGCCAGGATGCCCGGCTGGAG 780  
QY 781 CGGAGCGTCCGTCAGCGCTTCTCCCTGTGCAC 813  
Db 781 CGGAGCGTCCGTCAGCGCTTCTCCCTGTGCAC 813  
RESULT 7  
AA225375



ID	AAZ25375 standard; cDNA; 900 BP.
AC	AAZ25375;
DT	17-DEC-1999 (first entry)
DE	Human FLINT #1 nucleotide sequence.
KW	Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL; apoptosis; inflammation; cancer; diabetes; acute liver failure; sepsis; hepatitis; ischaemia-associated injury; hypercoagulation; refrusion-associated injury; aplastic anaemia; differentiation; growth; myelodysplastic syndrome; pancytopenic condition; myocardial ischaemia; ss.
XX	
OS	Homo sapiens.
PN	MO950413-A2.
XX	
PD	07-OCT-1999.
PF	30-MAR-1999; 99WO-US06797.
PR	30-MAR-1998; 98US-0079856. 30-MAY-1998; 98US-0086074. 09-SEP-1998; 98US-0099643. 17-DEC-1998; 98US-0112577. 18-DEC-1998; 98US-0112703. 18-DEC-1998; 98US-0112933. 22-DEC-1998; 98US-0113407.
PA	(ELIL ) LILLY & CO ELI.
PI	Bumol TF, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG, Hui KY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA, Song HY, Wang J, Wu X, Zuckerman SH;
PI	WPI: 1999-591319/50.
DR	P-PsDB; AA42182.
XX	
PT	Use of mature FLINT for treating acute liver failure, inflammation, cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic and proinflammatory activity
PS	Claim 28; Fig 1; 99pp; English.
XX	
CC	The present invention describes therapeutic applications of mature FLINT (mFLINT) for use in the treatment of acute liver failure. Mature FLINT (mFLINT), which is a member of the tumour necrosis factor receptor superfamily, is used for treating acute liver failure, inflammation of the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated injury or disorder such as hypercoagulation (including use with thrombolytic or anti-thrombolytic agents), reperfusion-associated injury or disorder, Type I diabetes, cancer, cell damage or damage to an innocent bystander tissue that is induced by a chemotherapeutic agent or therapeutic irradiation, treating haematopoietic progenitor cells that have been exposed to therapeutic radiation or chemotherapy, aplastic anaemia, myelodysplastic syndrome or a pancytopenic condition. mFLINT is also used for promoting the growth or differentiation of a haematopoietic progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte resulting from abnormal myocardial ischaemia. The present sequence encodes human FLINT.
SO	Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
QY	Query Match 100.0%; Score 813; DB 20; Length 900; Best Local Similarity 100.0%; Pred. No. 5,1e-145; Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 GTGGAGGAAGAACCACCACTTGTGGCGGAGCAGACAGAGGAGGAGGCTGTGTC 60 88 GTGGAGGAAGAACCACCACTTGTGGCGGAGCAGACAGAGGAGGAGGCTGTGTC 147

QY	61	GGCCAGTACCCCCAGAGCACTTTGTGCAGCGGCGCTGCGCCAGACAGACCCACGAC	120
Db	148	GGCCAGTACCCCCAGAGCACTTTGTGCAGCGGCGCTGCGCCAGACAGACCCACGAC	207
QY	121	TGTGGCCGCTGTCCACCGCGCACTACACGATTTCTGGAACTACCTTGAGCGCTGC	180
Db	208	TGTGGCCGCTGTCCACCGCGCACTACACGATTTCTGGAACTACCTTGAGCGCTGC	267
QY	151	TACTGCACGTCCTCTGGGGGAGACGTGAGAGGACACGGGCTTGCACCGCAC	247
Db	268	TACTGCACGTCCTCTGGGGGAGACGTGAGAGGACACGGGCTTGCACCGCAC	327
QY	241	AACCGTGCCTGCGCTGCGCCAGCGGCTTTCTCCGACAGCTGGATTTCTGTTGAGAC	300
Db	328	AACCGTGCCTGCGCTGCGCCAGCGGCTTTCTCCGACAGCTGGATTTCTGTTGAGAC	387
QY	301	GCATGTGTCCACCTGTGGCGCGGTATTTGCCCGGACACCCCGACCGAACCGCAG	366
Db	388	GCATGTGTCCACCTGTGGCGCGGTATTTGCCCGGACACCCCGACCGAACCGCAG	447
QY	351	TGGCAGCGCTGCCCCCGACGCACTTTCTCAGCCAGCAGCTTCAGCTCAGAGCACTGC	420
Db	448	TGGCAGCGCTGCCCCCGACGCACTTTCTCAGCCAGCAGCTTCAGCTCAGAGCACTGC	507
QY	421	CCCCACGCACTACACGCGCCCTGGGCGTGGCCCTCATGTGCGAGGCTCTTCCCTCC	480
Db	508	CCCCACGCACTACACGCGCCCTGGGCGTGGCCCTCATGTGCGAGGCTCTTCCCTCC	567
QY	481	GACACCTCTGTGCACCACTGCTGACTGGCTTCCCTCCAGCACCAAGGATCACAGAGCT	540
Db	568	GACACCTCTGTGCACCACTGCTGACTGGCTTCCCTCCAGCACCAAGGATCACAGAGCT	627
QY	541	GAGGTGAGCGCTGCGCTCATTCGATTTGTGGCTTTCCAGGACATCTCCATCCAGAGCT	600
Db	628	GAGGTGAGCGCTGCGCTCATTCGATTTGTGGCTTTCCAGGACATCTCCATCCAGAGCT	687
QY	601	CAGCGGCTGTGCAGAGGCGCTTCGAGGCGCCCGAGAGGCTGTCCGACACCAAGGCGG	666
Db	688	CAGCGGCTGTGCAGAGGCGCTTCGAGGCGCCCGAGAGGCTGTCCGACACCAAGGCGG	747
QY	661	CGCGCGGCTTGTGCAGCTGAAAGCTGCGTGGCGGCTTCAGGAGCTCTTGAGGCGCAG	720
Db	748	CGCGCGGCTTGTGCAGCTGAAAGCTGCGTGGCGGCTTCAGGAGCTCTTGAGGCGCAG	807
QY	721	GGGGCGCTGTGGGCGGCGCTGCGGCGCTGCGCGCTGCGCGAGATGCCCGGAGCTGAG	780
Db	808	GGGGCGCTGTGGGCGGCGCTGCGGCGCTGCGCGCTGCGCGAGATGCCCGGAGCTGAG	867
QY	781	CGAGCGCTGCTGAGCGCTTCTCTCTCTGTCAC	813
Db	868	CGAGCGCTGCTGAGCGCTTCTCTCTCTGTCAC	900
RESULT 8			
AAAS3208			
ID	AAAS3208 standard; cDNA; 900 BP.		
AC	AAAS3208;		
XX	03-JAN-2001 (first entry)		
DE	Human Fas ligand inhibitor FLINT coding sequence.		
XX	Human, Fas ligand inhibitor, FLINT; apoptosis; autoimmune disease;		
KW	inflammation; infectious disease; ischaemia; Alzheimer's disease;		
KW	Parkinson's disease; Crohn's disease; transplantation; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
FX	Homo sapiens.		
FT	Key		
CD	Location/Qualifiers		
FT	1..900		
FT	/*tag= a		

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FT FT /product= "FLINT"
FT FT /partial
FT FT 1..90
FT FT /*tag= b
FT FT 91..900
FT FT /*tag= c
FT FT
XX XX WO200034782-A1.
XX XX 15-JUN-2000.
XX XX 07-DEC-1999; 99WO-US28696.
XX XX 09-DEC-1998; 98US-0111575.
XX XX 09-DEC-1998; 98US-0111580.
XX XX 07-JAN-1999; 99US-0115069.
XX XX (ELIL ) LILLY & CO ELI.
XX XX Rostock PRJ, Song HY, Su EW;
XX XX WPI; 2000-431379/37.
XX XX P-PSDB; AAB03621.
XX XX Novel monkey Fas ligand inhibitor polypeptides, useful for treating
XX XX inflammatory or autoimmune disease such as rheumatoid arthritis,
XX XX infectious diseases such as chronic hepatitis, and
XX XX Ischaemia/Re-perfusion conditions -
XX XX Example 1; Page 88-91; 101pp; English.
XX XX
XX XX The present sequence is the coding sequence of the human Fas ligand
XX XX inhibitor (FLINT). The FLINT protein is involved in cell-specific
XX XX apoptosis, and can be used to treat inflammatory and autoimmune diseases
XX XX such as rheumatoid arthritis, inflammatory bowel disease,
XX XX graft-versus-host disease, diabetes, psoriasis and Graves' disease,
XX XX infectious diseases such as HIV-induced lymphopenia, fulminant viral
XX XX hepatitis B/C, chronic hepatitis and cirrhosis, and H. pylori-associated
XX XX ulceration, ischaemia and reperfusion conditions including acute
XX XX myocardial infarction, acute coronary syndrome, congestive heart failure
XX XX and atherosclerosis, and Alzheimer's and Parkinson's diseases, brain
XX XX injury and acute respiratory distress syndrome, Crohn's disease, aplastic
XX XX trauma and injury, chronic glomerulonephritis, osteoporosis, anemic
XX XX anaemia, myelodysplasia, ulcerative colitis, Down's syndrome, and
XX XX multiple sclerosis. In addition, the gene and protein can be used to
XX XX prevent apoptosis following organ transplantation.
XX XX
XX XX Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;
XX XX
XX XX Query Match 100.0%; Score 813; DB 21; Length 900;
XX XX Best Local Similarity 100.0%; Pred. No. 5.1e-145;
XX XX Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1 GTGCAGAAACCCACTACCTCCCTGGCGGACGACAGACAGGGGCGGCTGGTGC 60
XX DB 88 GTGCAGAAACCCACTACCTCCCTGGCGGACGACAGACAGGGGCGGCTGGTGC 147
XX QY 61 GCCCAGTGCCCCCAGGACCTTTGTGAGCGGCGGCGGCGGAGACAGCCCCCAGCAG 120
XX DB 148 GCCCAGTGCCCCCAGGACCTTTGTGAGCGGCGGCGGCGGAGACAGCCCCCAGCAG 207
XX QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTTGGAACTACCTGGAGCGGTGCCG 180
XX DB 208 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTTGGAACTACCTGGAGCGGTGCCG 267
XX QY 181 TACTGCAACGCTCTCTCGGGGAGCGTGGAGAGAGGACGCGGCTTCCAGCGCCACCCAC 240
XX DB 268 TACTGCAACGCTCTCTCGGGGAGCGTGGAGAGAGGACGCGGCTTCCAGCGCCACCCAC 327
XX QY 241 AACCGTCCCTGCGCGTCCGCGACCGGCTTCTTCGCGCACGCTGGTTTCTGTTGGAGCAC 300
XX DB 328 AACCGTCCCTGCGCGTCCGCGACCGGCTTCTTCGCGCACGCTGGTTTCTGTTGGAGCAC 387
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QY 301 GCATCGTGTCCACCTGGTCCCGGCGGATGTTGCCCGGGCACCCCGCAGCAGACGCGAG 360
DB 388 GCATCGTGTCCACCTGGTCCCGGCGGATGTTGCCCGGGCACCCCGCAGCAGACGCGAG 447
QY 361 TGCAGCCGTGCCCCCCCCAGGACCTTTCTCAGCCAGCAGCTCCAGCTCAGAGTAGTCCCGAG 420
DB 448 TGCAGCCGTGCCCCCCCCAGGACCTTTCTCAGCCAGCAGCTCCAGCTCAGAGTAGTCCCGAG 507
QY 421 CCCACCGCAACTGCACGGCCCTGGGCCCTCAATGTGCGCAGGCTCTTCTCTCCCAT 480
DB 508 CCCACCGCAACTGCACGGCCCTGGGCCCTCAATGTGCGCAGGCTCTTCTCTCCCAT 567
QY 481 GACACCTGTGCACAGCTGCACTGGCTTCCCTCAGCACAGGCTACCGAGGCTGAG 540
DB 568 GACACCTGTGCACAGCTGCACTGGCTTCCCTCAGCACAGGCTACCGAGGCTGAG 627
QY 541 GAGTGTGAGCGTGCCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 600
DB 628 GAGTGTGAGCGTGCCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGGCTG 687
QY 601 CAGCGCTGTGCAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGG 660
DB 688 CAGCGCTGTGCAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGG 747
QY 661 CGCGCGCTGTGCAGCTGAAGCTGCGTGGCGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGG 720
DB 748 CGCGCGCTGTGCAGCTGAAGCTGCGTGGCGGCTTCGAGGCTTCGAGGCTTCGAGGCTTCGAGG 807
QY 721 GGGGCGCTGTGCTGGTGGCTGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 780
DB 808 GGGGCGCTGTGCTGGTGGCTGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 867
QY 781 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCGAC 813
DB 868 CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCGAC 900
XX XX RESULT 9
XX XX ID AAA51075 standard; DNA; 900 BP.
XX XX AC AAA51075;
XX XX AC AAA51075;
XX XX 26-SEP-2000 (first entry)
XX XX Human FLINT coding sequence.
XX XX
XX FLINT; osteoprotegerin 3; OPG3; tumour necrosis factor receptor; TNFR;
XX FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotropic;
XX anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
XX anti-inflammatory; antibacterial; immunosuppressive; ds.
XX OS Homo sapiens.
XX XX Key Location/Qualifiers
XX CDS 1..900
XX FT /*tag= a
XX FT /product= FLINT
XX FT /partial
XX FT sig_peptide 1..87
XX FT /*tag= b
XX FT mat_peptide 88..900
XX FT /*tag= c
XX XX WO200037094-A2.
XX XX 29-JUN-2000.
XX XX 21-DEC-1999; 99WO-US30734.
XX XX 22-DEC-1998; 98US-0113407.
XX XX 30-MAR-1999; 99WO-US06797.
XX XX 20-OCT-1999; 99US-017239.
```

XX (BLI ) LILLY & CO ELI.  
 XX Cohen Fu, Posada JA, Wierda D;  
 XX WPI; 2000-475441/41.  
 DR P-PSDB; AAY96596.  
 XX  
 PT Use of mature FLINT for treating e.g. acute respiratory distress  
 PT syndrome, ulcerative colitis or ischemic injury during organ  
 PT transplantation  
 XX  
 PS Example 7, Fig 1A-B; 125pp; English.  
 XX  
 CC Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis  
 CC factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and  
 CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas  
 CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for  
 CC treating acute respiratory distress syndrome, creating or inhibiting  
 CC ulcerative colitis, inhibiting ischemic injury during organ  
 CC transplantation or for organ preservation during transplantation. mFLINT  
 CC can also be used to treat acute liver failure, inflammation of the liver,  
 CC abnormal (hepatocycle) apoptosis, sepsis, disorders associated with  
 CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,  
 CC damage to a cardiac myocyte resulting from abnormal myocardial ischaemia,  
 CC Type I diabetes, cancer, damage to an innocent bystander tissue induced  
 CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,  
 CC myelodysplastic syndromes and pancytopenic conditions.  
 XX  
 SO Sequence 900 BP; 128 A; 324 C; 304 G; 144 T; 0 other;  
 XX  
 Query Match 100.0%; Score 813; DB 21; Length 900;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-145;  
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGGCAGAAACACCCACTTACCTTGGCGGAGCGCAGAGACAGGAGCGGCTGTGTC 60  
 DB 88 GTGGCAGAAACACCCACTTACCTTGGCGGAGCGCAGAGACAGGAGCGGCTGTGTC 147  
 QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGAGGCGGCGCGCCGAGACAGCCCAAGAC 120  
 DB 148 GCCCAGTGGCCCCCAGGACCTTTGTGAGGCGGCGCGCCGAGACAGCCCAAGAC 207  
 QY 121 TGTGGCCCGTGTCCAGCGCGCACTTACAGGAGTTTGAATCTCTGGAGCGTGGCGG 180  
 DB 208 TGTGGCCCGTGTCCAGCGCGCACTTACAGGAGTTTGAATCTCTGGAGCGTGGCGG 267  
 QY 181 TACTGCAACGTCTCTCGGGGAGCGTGAGAGAGGACGCGGCTTCCAGCCACCCAC 240  
 DB 268 TACTGCAACGTCTCTCGGGGAGCGTGAGAGAGGACGCGGCTTCCAGCCACCCAC 327  
 QY 241 AACCGTGTCCCGCTGCGGACCGGCTTCTTGGCGACGCTGTGTTCTGTGGAGAC 300  
 DB 328 AACCGTGTCCCGCTGCGGACCGGCTTCTTGGCGACGCTGTGTTCTGTGGAGAC 387  
 QY 301 GCATCGTGTCCACTGTGTCGGCGGATTTGCCGGGCAACCCACAGCAAGACCGCAG 360  
 DB 388 GCATCGTGTCCACTGTGTCGGCGGATTTGCCGGGCAACCCACAGCAAGACCGCAG 447  
 QY 361 TGCAGGCGTGGCCCCCAGGACCTTCTCAGCCAGCAGCTTCACAGCATGCGCAG 420  
 DB 448 TGCAGGCGTGGCCCCCAGGACCTTCTCAGCCAGCAGCTTCACAGCATGCGCAG 507  
 QY 421 CCCACCGCACTGACAGCGCCCTTGGGCTTCCATATGTGCCAGGCTTCTTCCCAT 480  
 DB 508 CCCACCGCACTGACAGCGCCCTTGGGCTTCCATATGTGCCAGGCTTCTTCCCAT 567  
 QY 481 GACACCGTGTGCACTGACAGCTTCCCTCAGCAACAGGATACCAAGAGCTGAG 540  
 DB 568 GACACCGTGTGCACTGACAGCTTCCCTCAGCAACAGGATACCAAGAGCTGAG 627  
 QY 541 GAGTGTAGGCGTGGCTGATGACTTTTGGCTTTCAGAGCATCTCATCAAGAGCTG 600

DB 628 GAGTGTAGGCGTGGCTGATGACTTTTGGCTTTCAGAGCATCTTCATCAAGAGCTG 687  
 QY 601 CAGCGGCTGTGAGGCGCCCTCGAGGCGCCCGAGAGGCTGGGCTCCGACACCAAGGCGGCG 660  
 DB 688 CAGCGGCTGTGAGGCGCCCTCGAGGCGCCCGAGAGGCTGGGCTCCGACACCAAGGCGGCG 747  
 QY 661 CCGCGGCGCTTGGACGTGAAGCTGCGTGGCGGCTCAAGAGCTCTGGGAGCGCAGAGC 720  
 DB 748 CCGCGGCGCTTGGACGTGAAGCTGCGTGGCGGCTCAAGAGCTCTGGGAGCGCAGAGC 807  
 QY 721 GGGGCGCTGTGCTGTGCGGCTGTGCAAGCGCTCGCGGTGCGCAGATGCCGAGCTGAG 780  
 DB 808 GGGGCGCTGTGCTGTGCGGCTGTGCAAGCGCTCGCGGTGCGCAGATGCCGAGCTGAG 867  
 QY 781 CGGAGCGTCCGTGAGGCGCTTCCCTCGTGCAC 813  
 DB 868 CGGAGCGTCCGTGAGGCGCTTCCCTCGTGCAC 900  
 XX  
 RESULT 10  
 ID AAX22300 standard; DNA; 903 BP.  
 XX  
 AC AAX22300;  
 XX  
 DT 20-MAY-1999 (first entry)  
 DE Orphan receptor (HUMAN NTR-1) polypeptide encoding DNA.  
 XX  
 XX HUMAN NTR-1; orphan receptor; osteoprotegerin; OPG; TNFR; human;  
 KM tumour necrosis factor receptor; muscle disorder; bone mass; screening;  
 KM muscle metabolism; binding agent; cognate ligand; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9907738-A2.  
 XX  
 PD 18-FEB-1999.  
 XX  
 PF 04-AUG-1998; 98WO-US16202.  
 XX  
 PR 06-AUG-1997; 97US-0054869.  
 XX  
 PA (PROC ) PROCTER & GAMBLE CO.  
 PA (REG-) REGENERON PHARM INC.  
 XX  
 PI Maslakowski PJ, Morris J, Valenzuela DM;  
 DR WPI; 1999-167365/14.  
 DR P-PSDB; AAW95082.  
 XX  
 PT Novel orphan human receptor polypeptide and nucleic acid - useful as  
 PT diagnostic reagents and for treatment of muscle disorders  
 XX  
 PS Claim 2; Page 21; 23pp; English.  
 XX  
 CC This DNA encodes a HUMAN NTR-1 polypeptide, a novel orphan receptor. The  
 CC protein is related to osteoprotegerin (OPG) and to tumour necrosis factor  
 CC receptor (TNFR). Host cells transformed with a vector comprising the  
 CC HUMAN NTR-1 nucleic acid are used for the recombinant expression of the  
 CC protein. HUMAN NTR-1 proteins and antibodies immuno specific for the  
 CC protein are useful for diagnosis and treatment of humans and animals,  
 CC especially muscle disorders, as the receptor is involved in regulation of  
 CC bone mass and muscle metabolism. HUMAN NTR-1 receptors are also useful  
 CC for screening for novel binding agents, and cognate ligands, which may be  
 CC used to treat disorders associated with HUMAN NTR-1 imbalance.  
 XX  
 SO Sequence 903 BP; 129 A; 324 C; 305 G; 145 T; 0 other;  
 XX  
 Query Match 100.0%; Score 813; DB 20; Length 903;  
 Best Local Similarity 100.0%; Pred. No. 5,1e-145;  
 Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCGAGAAACACCCACCTTACCCCTGGGGGAGCCAGAGACAGGGAGCGCTGGTGTGC 60  
Db GTGCGAGAAACACCCACCTTACCCCTGGGGGAGCCAGAGACAGGGAGCGCTGGTGTGC 147  
QY 61 GCCCAGTGGCCCCCAGAGCAGCTTTGTGACGGCCGTGGCCGAGAGACAGCCACGACG 120  
Db 148 GCCCAGTGGCCCCCAGAGCAGCTTTGTGACGGCCGTGGCCGAGAGACAGCCACGACG 207  
QY 121 TGTGGCCGCTGTCCACCGCGCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 180  
Db 208 TGTGGCCGCTGTCCACCGCGCACTACACGAGTTCTGGAACTACCTGGAGCGCTGCCGC 267  
QY 181 TACTGCAACGTCCTCTGCGGGAGCGTGAAGAGAGCAAGGGCTTGCAGCGCCACCCAC 240  
Db 268 TACTGCAACGTCCTCTGCGGGAGCGTGAAGAGAGCAAGGGCTTGCAGCGCCACCCAC 327  
QY 241 AACCGTCCCTGCGCTGCGGACCGCTTCTTCCGACAGCGTGTCTTCTGTTGGAGCAC 300  
Db 328 AACCGTCCCTGCGCTGCGGACCGCTTCTTCCGACAGCGTGTCTTCTGTTGGAGCAC 387  
QY 301 GCATCGTGTCCACCTGCTGGCGGCTGATTGCCCCGGGACACCCCGAGCAAGACGACG 360  
Db 388 GCATCGTGTCCACCTGCTGGCGGCTGATTGCCCCGGGACACCCCGAGCAAGACGACG 447  
QY 361 TGCAGCGCTGCCCCCAGGACCTTCTCAGCCAGAGCTTCCAGCTCAGAGCAGTGCAG 420  
Db 448 TGCAGCGCTGCCCCCAGGACCTTCTCAGCCAGAGCTTCCAGCTCAGAGCAGTGCAG 507  
QY 421 CCCCACCGCAACTGCAGCGCCCTGGGCTGCGGCTCAATGTGCCAGGCTTCTTCCCTCAT 480  
Db 508 CCCCACCGCAACTGCAGCGCCCTGGGCTGCGGCTCAATGTGCCAGGCTTCTTCCCTCAT 567  
QY 481 GACACCTGTGCACAGCTGACCTGGCTTCCCTCAGCAGCGGTACAGGAGCTGAG 540  
Db 568 GACACCTGTGCACAGCTGACCTGGCTTCCCTCAGCAGCGGTACAGGAGCTGAG 627  
QY 541 GAGTGTAGCGTGGCGTCAATCGATTTGTGGCTTTCAGGACATCTCCATCAAGAGCTG 600  
Db 628 GAGTGTAGCGTGGCGTCAATCGATTTGTGGCTTTCAGGACATCTCCATCAAGAGCTG 687  
QY 601 CAGCGCTGTGCAGGCGCTCAGGCGCCCGAGGCGTGGGTCCGACACCAAGGCGCGGC 660  
Db 688 CAGCGCTGTGCAGGCGCTCAGGCGCCCGAGGCGTGGGTCCGACACCAAGGCGCGGC 747  
QY 661 CGCGCGCTTTCAGCTCAAGCTCGTGGCGCTCAGGAGCTTCTGGGGCGCAGGAC 720  
Db 748 CGCGCGCTTTCAGCTCAAGCTCGTGGCGCTCAGGAGCTTCTGGGGCGCAGGAC 807  
QY 721 GGGCGCTGTGTGGCGCTCTCAGCGCTGCGGCTCAGGAGTCCCGGCTGGAG 780  
Db 808 GGGCGCTGTGTGGCGCTCTCAGCGCTGCGGCTCAGGAGTCCCGGCTGGAG 867  
QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813  
Db 868 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 900

RESULT 11

AAF62705  
ID AAF62705 standard; cDNA; 1055 BP.  
XX  
AC AAF62705;  
XX  
XX 02-MAY-2001 (first entry)  
XX Human NTR3 nucleotide sequence.  
DE Human, NTR3; tumour necrosis factor receptor; TNF receptor; anti-HIV;  
KW antianemic; immunosuppressive; antidiabetic; antiviral; antibacterial;  
KW cytosolic; neuroprotective; antiinflammatory; anorectic; vasotropic;  
KW antirheumatoid; antiarthritic; cerebroprotective; tuberculostatic;  
KW gene therapy; cancer; blood disorder; brain disorder; autoimmune disease;  
KW infection; .

XX Homo sapiens.  
XX WO200110908-A1.  
XX 15-FEB-2001.  
XX 02-AUG-2000; 2000WO-US21287.  
XX 04-AUG-1999; 99US-0147297.  
XX (AMGB-) AMGEN INC.  
XX Hsu H;  
XX WPI; 2001-191521/19.  
XX P-PSDB; AAB71754.  
XX New tumor necrosis factor receptor, NTR3, useful for treating cancers,  
XX stroke, anemia, obesity, rheumatoid arthritis and transplantation  
XX rejection -  
XX Claim 1; Page 128-129; 135pp; English.  
XX The present sequence encodes the tumour necrosis factor (TNF) receptor  
XX polypeptide NTR3. The NTR3 polynucleotides and polypeptides are useful  
XX for treating diseases such as acquired-immunodeficiency syndrome (AIDS),  
XX anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria,  
XX diabetes mellitus, disseminated intravascular coagulopathy, erythroid  
XX sick syndrome, haemorrhagic shock, hepatitis, insulin resistance,  
XX leprosy, leukaemia, meningitis, multiple sclerosis, myocardial ischaemia,  
XX obesity, rejection of transplanted organs, rheumatoid arthritis, septic  
XX shock syndrome, stroke, adult respiratory distress syndrome (ARDS),  
XX tuberculosis, and a number of viral diseases. The NTR3 polypeptide is  
XX useful for identifying or developing new (ant)agonists of NTR3. It may  
XX be used as an immunogen to which antibodies may be raised. NTR3 nucleic  
XX acid molecules may be useful as hybridisation probes in diagnostic assays  
XX to test, either qualitatively or quantitatively, for the presence of an  
XX NTR3 DNA or corresponding RNA in mammalian tissue or bodily fluid  
XX samples.  
XX  
SQ Sequence 1055 BP; 160 A; 369 C; 340 G; 186 T; 0 other;  
Query Match 100.0%; Score 813; DB 22; Length 1055;  
Best Local Similarity 100.0%; Pred. NO. 5.1e-145;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGCGAGAAACACCCACCTTACCCCTGGGGGAGCCAGAGACAGGGAGCGCTGGTGTGC 60  
Db 154 GTGCGAGAAACACCCACCTTACCCCTGGGGGAGCCAGAGACAGGGAGCGCTGGTGTGC 213  
QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGGCCGTGGCCGAGAGACAGCCACGACG 120  
Db 214 GCCCAGTGGCCCCCAGGACCTTTGTGACGGCCGTGGCCGAGAGACAGCCACGACG 273  
QY 121 TGTGGCCGCTGTCCACCGCGCACTACACGAGTTCTTGGAACTACCTGGAGCGCTGCCGC 180  
Db 274 TGTGGCCGCTGTCCACCGCGCACTACACGAGTTCTTGGAACTACCTGGAGCGCTGCCGC 333  
QY 181 TACTGCAACGTCCTCTGCGGGAGCGTGAAGAGAGCAAGGGCTTGCAGCGCCACCCAC 240  
Db 334 TACTGCAACGTCCTCTGCGGGAGCGTGAAGAGAGCAAGGGCTTGCAGCGCCACCCAC 393  
QY 241 AACCGTCCCTGCGCTGCGGACCGCTTCTTCCGACAGCGTGTCTTCTGTTGGAGCAC 300  
Db 394 AACCGTCCCTGCGCTGCGGACCGCTTCTTCCGACAGCGTGTCTTCTGTTGGAGCAC 453  
QY 301 GCATCGTGTCCACCTGCTGGCGGCTGATTGCCCCGGGACACCCCGAGCAAGACGACG 360  
Db 454 GCATCGTGTCCACCTGCTGGCGGCTGATTGCCCCGGGACACCCCGAGCAAGACGACG 513  
QY 361 TGCAGCGCTGCCCCCAGGACCTTCTCAGCCAGAGCTTCCAGCTCAGAGCAGTGCAG 420

Db 514 TGCCAGCCGTCGCCCCAGGACCTTCTCAGCCAGAGCTTCAGCTGAGAGCTGCCAG 573  
QY 421 CCCACCGCAACTGACAGGCGCTGGGCTGGGCTGCAATGATGCCAGGCTTCTCCCAT 480  
Db 574 CCCACCGCAACTGACAGGCGCTGGGCTGGGCTGCAATGATGCCAGGCTTCTCCCAT 633  
QY 481 GACACCTGTGACACGAGCTGAGCTTCCCTCAGACACAGGATGACAGAGCTGAG 540  
Db 634 GACACCTGTGACACGAGCTGAGCTTCCCTCAGACACAGGATGACAGAGCTGAG 693  
QY 541 GAGGTGATGAGTGGCGCTGATGATTTGTGCTTCCAGACATCTCATCAAGAGCTG 600  
Db 694 GAGGTGATGAGTGGCGCTGATGATTTGTGCTTCCAGACATCTCATCAAGAGCTG 753  
QY 601 CAGCGCTGTGACAGGCGCTGAGGCGCCGAGAGGCTGGGGTCCGACACCAAGGCGGCG 660  
Db 754 CAGCGCTGTGACAGGCGCTGAGGCGCCGAGAGGCTGGGGTCCGACACCAAGGCGGCG 813  
QY 661 CCGCGGCGCTTGCAGCTGAAGCTGCGTGGCGGCTCAAGAGCTCTTGGGGCGCAGAGAC 720  
Db 814 CCGCGGCGCTTGCAGCTGAAGCTGCGTGGCGGCTCAAGAGCTCTTGGGGCGCAGAGAC 873  
QY 721 GGGGCGCTGCTGTGTCGGCGCTGCTCAGGCGCTGCGCTGGCAGAGATCCCGGCTGAG 780  
Db 874 GGGGCGCTGCTGTGTCGGCGCTGCTCAGGCGCTGCGCTGGCAGAGATCCCGGCTGAG 933  
QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTCAC 813  
Db 934 CGAGCGTCCGTGAGCGCTTCTCCCTGTCAC 966

RESULT 12  
AAAS3802  
ID AAAS3802 standard; cDNA; 1066 BP.  
AC AAAS3802;  
XX  
DT 19-DEC-2000 (First entry)

DE M68 TNF receptor related protein coding sequence.  
XX  
XX

KM M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;  
KM receptor; immune response; cell differentiation; ligand; cancer;  
KM bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;  
KM Grave's disease; idiopathic myxedema; autoimmune diabetes;  
KM thrombotic thrombocytopenic purpura; multiple sclerosis;  
KM liver diseases; autoimmune gastritis; ulcerative colitis;  
KM glomerulonephritis; pulmonary fibrosis; heart failure;  
KM atherosclerosis; aplastic anaemia; myelodysplastic syndromes;  
KM osteoporosis; Alzheimer's disease; Parkinson's disease; stroke;  
KM myocardial infarction; human; ds.

XX Homo sapiens.

OS  
FH Key Location/Qualifiers  
FT CDS 53..955  
FT /tag= a  
FT /product= M68 polypeptide

PN MO200046247-A1.

PD 10-AUG-2000.

PF 04-FEB-2000; 2000MO-US03037.

PR 05-FEB-1999; 99US-0118902.

PR 20-DEC-1999; 99US-0172754.

XX (MERI ) MERCK & CO INC.

XX Bai C;

XX WPI; 2000-506066/45.

DR P-PSDB; AAY97246.  
XX  
PT Isolated human M68 nucleic acids and proteins which are part of the  
PT tumor necrosis factor receptor (TNFR) family; useful for identifying  
PT modulators that may be used to treat various diseases e.g. cancer,  
PT osteoporosis, Alzheimer's disease  
XX  
PS Claim 21; Page 73-75; 80bp; English.  
XX  
CC The M68 protein is a member of a family of proteins which have  
CC roles in immune responses, cell death, cell proliferation and  
CC stimulation of cell differentiation. M68 lacks a transmembrane domain  
CC and is a secreted factor suggesting that it functions as a natural  
CC inhibitor for its ligand. The altered expression pattern of M68 in a  
CC multitude of tissues suggests that M68 may play a role in cancer by  
CC binding to its ligand and blocking apoptotic cell death induced by  
CC such a ligand. This anti-apoptotic role of M68 suggests that  
CC modulators of M68 will be useful in treatment of apoptosis-related  
CC diseases such as various forms of cancer and various bone disorders.  
CC M68 nucleic acids and proteins are therefore useful for treating  
CC conditions involving atypical apoptosis and for identifying  
CC modulators of M68. Modulators of M68 are useful for treatment of  
CC cancer and other diseases associated with abnormal levels of  
CC apoptosis including systemic lupus erythematosus, Hashimoto's  
CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune  
CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,  
CC liver diseases, autoimmune gastritis, ulcerative colitis,  
CC glomerulonephritis, pulmonary fibrosis, heart failure,  
CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,  
CC osteoporosis, Alzheimer's disease, Parkinson's disease, stroke, and  
CC myocardial infarction.  
XX

SO Sequence 1066 BP; 178 A; 367 C; 335 G; 186 T; 0 other;

Query Match 100.0%; Score 813; DB 21; Length 1066;  
Best Local Similarity 100.0%; Pred. No. 5.1e-145;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAAAACACCCCTTACCCCTGGCGGAGACAGACACAGGGAGCGGCTGTGTC 60  
Db 140 GTGGCAAAACACCCCTTACCCCTGGCGGAGACAGACAGGGAGCGGCTGTGTC 199  
QY 61 GCCAGTGGCCCCCAGGACCTTTGTGACGGCGCGTGGCGGAGACAGCCCCAGAG 120  
Db 200 GCCAGTGGCCCCCAGGACCTTTGTGACGGCGCGTGGCGGAGACAGCCCCAGAG 259  
QY 121 TGTGGCCGTGTTCACCGCGCACTACAGCAGTTCTGAACTTACCTGAGCCGTCGG 180  
Db 260 TGTGGCCGTGTTCACCGCGCACTACAGCAGTTCTGAACTTACCTGAGCGCTCGCG 319  
QY 181 TACTGCAAGTCTCTTGGCGGAGGCTGAGAGAGGACAGGCGCTTCCAGCGCACCC 240  
Db 320 TACTGCAAGTCTCTTGGCGGAGGCTGAGAGAGGACAGGCGCTTCCAGCGCACCC 379  
QY 241 AACGTCGCTGCGGCTGCGGACACGGCTTCTTGGCGACAGCTGTTCTGCTTGGAGAC 300  
Db 380 AACGTCGCTGCGGCTGCGGACACGGCTTCTTGGCGACAGCTGTTCTGCTTGGAGAC 439  
QY 301 GCATGTGTTCACCTGTGCGGCGGTGATTTGCCCGGACACCCCAAGCAACAGCGAG 360  
Db 440 GCATGTGTTCACCTGTGCGGCGGTGATTTGCCCGGACACCCCAAGCAACAGCGAG 499  
QY 361 TGGCAGCGTGGCCCCCAGGACCTTCTCAGCGACAGCTCCAGCTTCAGAGAGTGGCAG 420  
Db 500 TGGCAGCGTGGCCCCCAGGACCTTCTCAGCGACAGCTCCAGCTTCAGAGAGTGGCAG 559  
QY 421 CCCACCGCAACTGACAGGCGCTGGGCTGGGCTGCAATGTGCAAGCTTCTCCCAT 480  
Db 560 CCCACCGCAACTGACAGGCGCTGGGCTGGGCTGCAATGTGCAAGCTTCTCCCAT 619  
QY 481 GACACCTGTGACACGAGCTGAGCTTCCCTCAGACACAGGATGACAGAGCTGAG 540  
Db 620 GACACCTGTGACACGAGCTGAGCTTCCCTCAGACACAGGATGACAGAGCTGAG 679

QY 541 GAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 600  
DB 680 GAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 739  
QY 601 CAGCGCTGTGACAGGCGCTTCGAGGCGCCCGAGGCGTGGGGTCCGACACCAAGGCGGGC 660  
DB 740 CAGCGCTGTGACAGGCGCTTCGAGGCGCCCGAGGCGTGGGGTCCGACACCAAGGCGGGC 799  
QY 661 CGCGCGCGCTTGACGTGAAGCTGCGTGGCGGCTCACGGAGTCTCTGGGGGCGCAGGAC 720  
DB 800 CGCGCGCGCTTGACGTGAAGCTGCGTGGCGGCTCACGGAGTCTCTGGGGGCGCAGGAC 859  
QY 721 GGGGCGCTGTGTCGGCTGTGTCAGGCGCTGCGGCTGCGCAGGATGCCGGGCTGGAG 780  
DB 860 GGGGCGCTGTGTCGGCTGTGTCAGGCGCTGCGGCTGCGCAGGATGCCGGGCTGGAG 919  
QY 781 CGGAGCGTCCGTGAGGCGTTCCTCCCTGTGCAC 813  
DB 920 CGGAGCGTCCGTGAGGCGTTCCTCCCTGTGCAC 952  
  
RESULT 13  
AAV39085  
ID AAV39085 standard; cDNA; 1077 BP.  
XX  
AC AAV39085;  
XX  
DT 26-OCT-1998 (first entry)  
XX  
DE Human tumour necrosis factor receptor-6 alpha cDNA.  
XX  
KW Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;  
KW endothelial cells; keratinocytes; normal prostate; apoptosis;  
KW prostate tumour tissue; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT 25..927  
FT CDS  
FT /\*tag= a  
FT /product= "TNFR-6 alpha protein"  
FT sig\_peptide 25..114  
FT /\*tag= b  
FT mat\_peptide 115..924  
FT /\*tag= c  
XX  
XX WO9830694-A2.  
XX  
XX 16-JUL-1998.  
XX  
XX 13-JAN-1998; 98WO-US00153.  
XX  
XX 14-JAN-1997; 97US-0035496.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;  
XX  
XX WPI; 1998-399142/34.  
XX P-PSDB; AAW63622.  
XX  
XX Human tumour necrosis factor receptors 6-alpha and 6-beta - used in  
XX the diagnosis of immune system-related disorder(s)  
XX  
XX Disclosure; Fig 1; 91pp; English.  
XX  
XX The present sequence represents the human tumour necrosis factor  
XX receptor-6 alpha (TNFR-6 alpha) cDNA. The invention also provides  
XX for the TNFR-6 beta cDNA (AAV39086). TNFR-6 alpha and TNFR-6 beta are  
XX members of the tumour necrosis factor receptor (TNFR) family. TNFRs  
XX are expressed in endothelial cells, keratinocytes, normal prostate and  
XX prostate tumour tissue. For a number of disorders of these cells,

CC particularly of the immune system, substantially altered (whether  
CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene  
CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta  
CC polypeptides, nucleic acids and antibodies are claimed to be useful in  
CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and  
CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are  
CC also claimed to be useful for identifying ligands which may be useful  
CC in the treatment of apoptosis related disorders.  
XX  
SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;  
  
Query Match 100.0%; Score 813; DB 19; Length 1077;  
Best Local Similarity 100.0%; Pred. No. 5.1e-145;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGGCAGAAACCCACCTTACCCCTGGCGGACGACAGACAGGAGCGGTGTGTGC 60  
DB 112 GTGGCAGAAACCCACCTTACCCCTGGCGGACGACAGACAGGAGCGGTGTGTGC 171  
QY 61 GCCCAGTGCCTCCAGGACCTTTGTGACGGCGCTGCGCGGACAGACAGCCACGACG 120  
DB 172 GCCCAGTGCCTCCAGGACCTTTGTGACGGCGCTGCGCGGACAGACAGCCACGACG 231  
QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGCACTTCTGAACTTACCTGGAGCGCTGCCG 180  
DB 232 TGTGGCCCGTGTCCACCGCGCCACTACACGCACTTCTGAACTTACCTGGAGCGCTGCCG 291  
QY 181 TACTGCAACGTCCTCTGTGGGGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
DB 292 TACTGCAACGTCCTCTGTGGGGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 351  
QY 241 AACCGTGCCTGCGGTGCGCGACCGGCTTCTTCGCGCAGCGCTGTTCTCTGTTGGAGC 300  
DB 352 AACCGTGCCTGCGGTGCGCGACCGGCTTCTTCGCGCAGCGCTGTTCTCTGTTGGAGC 411  
QY 301 GCATCGTGTCCACCTGGTGCCTGCGGTGATTTGCCCGGCGACCCCGGAGCAGACGCGAG 360  
DB 412 GCATCGTGTCCACCTGGTGCCTGCGGTGATTTGCCCGGCGACCCCGGAGCAGACGCGAG 471  
QY 361 TGCAGCGTGTGCCCCCAGGACCTTCTCAGCGCAGCGTCCAGCTCAGAGAGTGCAG 420  
DB 472 TGCAGCGTGTGCCCCCAGGACCTTCTCAGCGCAGCGTCCAGCTCAGAGAGTGCAG 531  
QY 421 CCCCACGCAACTGACGCGCGCTGCGGCTTCAATGTGCGCAGGCTTCTTCTCCCAT 480  
DB 532 CCCCACGCAACTGACGCGCGCTGCGGCTTCAATGTGCGCAGGCTTCTTCTCCCAT 591  
QY 481 GACACCTGTGCACACGCTGCACTGGCTTCCCGCTCAGCACGAGGTACGAGAGCTGAG 540  
DB 592 GACACCTGTGCACACGCTGCACTGGCTTCCCGCTCAGCACGAGGTACGAGAGCTGAG 651  
QY 541 GAGTGTGAGCGTGCCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 600  
DB 652 GAGTGTGAGCGTGCCTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGGCTG 711  
QY 601 CAGCGCTGTGACGCGCTTCGAGGCGCCCGAGGCGTGGGGTCCGACACCAAGGCGGGC 660  
DB 712 CAGCGCTGTGACGCGCTTCGAGGCGCCCGAGGCGTGGGGTCCGACACCAAGGCGGGC 771  
QY 661 CAGCGCGCTTGCAGCTGAAGCTGCGTCCGCGGCTCACGAGCTCTCGGGGCGCAGGAC 720  
DB 772 CAGCGCGCTTGCAGCTGAAGCTGCGTCCGCGGCTCAGGAGCTCTCGGGGCGCAGGAC 831  
QY 721 GGGGCGCTGTGTCGGCTGTGTCAGGCGCTGCGGTGCCAGGATGCCGGGCTGGAG 780  
DB 832 GGGGCGCTGTGTCGGCTGTGTCAGGCGCTGCGGTGCCAGGATGCCGGGCTGGAG 891  
QY 781 CGGAGCGTCCGTGAGGCGTTCCTCCCTGTGCAC 813  
DB 892 CGGAGCGTCCGTGAGGCGTTCCTCCCTGTGCAC 924  
  
RESULT 14

AAA37772  
ID AAA37772 standard; DNA; 1077 BP.  
XX  
AC AAA37772;  
XX  
DT 04-DEC-2000 (first entry)  
XX  
DE Human tumour necrosis factor receptor-6 alpha coding sequence.  
XX  
KW Human; Tumour necrosis factor receptor 6; TNFR-6alpha; TNFR-6beta;  
KW ocular neovascularisation; solid tumour; malignancy; prostate cancer;  
KW breast cancer; colon cancer; diabetic retinopathy; microbial infection;  
KW pre-maturity macular degeneration; allergy; inflammation; tissue damage;  
KW thyroid associated ophthalmopathy; cell damage; parasitic infection;  
KW bone disease; osteoporosis; atherosclerosis; cardiovascular disease;  
KW neurodegenerative disorder; Alzheimer's disease; immune disorder;  
KW graft rejection; rheumatism; liver disease; autoimmune diabetes; asthma;  
KW psoriasis; septic shock; ulcerative colitis; therapy; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 25..927  
FT /\*tag= a  
FT /product= TNFR-6alpha  
XX  
PN MO200052028-A1.  
XX  
PD 08-SEP-2000.  
XX  
PF 03-MAR-2000; 2000MO-US05686.  
XX  
PR 04-MAR-1999; 99US-012174.  
PR 12-MAR-1999; 99US-0124092.  
PR 27-APR-1999; 99US-0131279.  
PR 30-APR-1999; 99US-0131964.  
PR 02-AUG-1999; 99US-0146371.  
PR 01-DEC-1999; 99US-0168235.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Gentz RL, Ni J, Ebner R, Yu G, Ruben SM, Feng P;  
XX  
DR WPI: 2000-572174/53.  
DR P-PSDB; AAY90357.  
XX  
PT Nucleic acids encoding human tumour necrosis factor receptor (TNFR)  
PT protein TNFR-6alpha and TNFR-6beta, useful for treating e.g.  
PT Alzheimer's disease, osteoporosis and graft rejection -  
XX  
PS Claim 2, Fig 1, 332pp; English.  
XX  
CC This sequence encodes the human tumour necrosis factor receptor 6  
CC alpha (TNFR-6alpha) of the invention. The TNFR-6alpha and TNFR-6beta DNA  
CC and protein sequences can be used in the prevention, treatment and  
CC diagnosis of diseases associated with inappropriate TNFR expression. The  
CC nucleic acids, polypeptides, antibodies, agonists and antagonists against  
CC them may be used for the treatment of a range of conditions such as  
CC disorders associated with neovascularisation (especially ocular  
CC neovascularisation) (such as solid tumours and malignancies (e.g.  
CC prostate cancer, breast cancer and colon cancer), diabetic retinopathy  
CC and pre-maturity macular degeneration), allergies, inflammation,  
CC thyroid associated ophthalmopathy (tissue/cell damage, wounds, microbial  
CC and parasitic infections, bone disease (e.g. osteoporosis),  
CC atherosclerosis, pain, cardiovascular disease (e.g. stroke),  
CC neurodegenerative disorders (e.g. Alzheimer's disease), immune  
CC disorders (e.g. graft rejection), rheumatism, liver disease,  
CC autoimmune diabetes, asthma, psoriasis, septic shock and ulcerative  
CC colitis.  
XX  
SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;  
Query Match 100.0%; Score 813; DB 21; Length 1077;

Best Local Similarity 100.0%; Pred. No. 5.1e-145;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGGCAAAACACCCACTACCCCTGGCGGAGACGAGAGACAGGGAGGGCTGGTGC 60  
DB 112 GTGGCAAAACACCCACTACCCCTGGCGGAGACGAGAGACAGGGAGGGCTGGTGC 171  
QY 61 GCCCAGTGGCCCCCAGAGCACTTTGTGACAGCGCGTGGCCGCGAGACAGCCCCAGACG 120  
DB 172 GCCCAGTGGCCCCCAGAGCACTTTGTGACAGCGCGCTGGCCGCGAGACAGCCCCAGACG 231  
QY 121 TGTGGCCCGTGTCCACCGGCGCACTACAGCAGTTTGTGAATTACTTGAGCCCTGCGCG 180  
DB 232 TGTGGCCCGTGTCCACCGGCGCACTACAGCAGTTTGTGAATTACTTGAGCCCTGCGCG 291  
QY 181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGAGAGAGACAGGGCTTGCACGCGACCCAC 240  
DB 292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGAGAGAGACAGGGCTTGCACGCGACCCAC 351  
QY 241 AACCGTGCCTGCGCGCTGCGCACCGGCTTCTTGGCGCACCGCTTCTTGGAGACAC 300  
DB 352 AACCGTGCCTGCGCGCTGCGCACCGGCTTCTTGGCGCACCGCTTCTTGGAGACAC 411  
QY 301 GCATGCTGTCCACCTGATGCGGCGGTGATTGCCCGGAGACCCCGAGCAACAGCAG 360  
DB 412 GCATGCTGTCCACCTGATGCGGCGGTGATTGCCCGGAGACCCCGAGCAACAGCAG 471  
QY 361 TGGCAGCCGTGCCCCCAGAGCACTTCTCAGCGACGACTCCAGCTCAGAGCTGCGAG 420  
DB 472 TGGCAGCCGTGCCCCCAGAGCACTTCTCAGCGACGACTCCAGCTCAGAGCTGCGAG 531  
QY 421 CCCACCGCAACTGACAGGCGCTGGGCTGGGCTGAGCTCATGTGCAAGGCTTCTCTCCAT 480  
DB 532 CCCACCGCAACTGACAGGCGCTGGGCTGGGCTGAGCTCATGTGCAAGGCTTCTCTCCAT 591  
QY 481 GACACCTGTGACACAGCTGCACTGCTTCCCTCAGACACAGGGTACAGAGAGCTGAG 540  
DB 592 GACACCTGTGACACAGCTGCACTGCTTCCCTCAGACACAGGGTACAGAGAGCTGAG 651  
QY 541 GAGTGTAGAGCTGCGCTGATGACATTGTGGCTTTCCAGACATCTTCATCAAGAGCTG 600  
DB 652 GAGTGTAGAGCTGCGCTGATGACATTGTGGCTTTCCAGACATCTTCATCAAGAGCTG 711  
QY 601 CAGCGGCTGTGACAGGCGCTCGAGGCGCCGAGAGGCTGGGGTCCGACACCAAGGGCGGG 660  
DB 712 CAGCGGCTGTGACAGGCGCTCGAGGCGCCGAGAGGCTGGGGTCCGACACCAAGGGCGGG 771  
QY 661 CGCGCGGCTTGGACGCTGAGCTGCGTGGCGGCTCACGAGGCTCTTGGGGGCGAGAGC 720  
DB 772 CGCGCGGCTTGGACGCTGAGCTGCGTGGCGGCTCACGAGGCTCTTGGGGGCGAGAGC 831  
QY 721 GGGGCGCTGCTGTGTGCGGCTGTGACAGGCGCTGCGGCTGCGGATGCGGGCTGGAG 780  
DB 832 GGGGCGCTGCTGTGTGCGGCTGTGACAGGCGCTGCGGCTGCGGATGCGGGCTGGAG 891  
QY 781 CGGAGGCTGCGTGAAGGCTTCTCCCTGAGCAG 813  
DB 892 CGGAGGCTGCGTGAAGGCTTCTCCCTGAGCAG 924  
RESULT 15  
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ID AAD33281 standard; cDNA; 1077 BP.  
XX  
AC AAD33281;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE Human tumour necrosis factor receptor (TNFR)-6alpha cDNA.  
XX  
KW Human; tumour necrosis factor receptor; TNFR-6alpha; TNFR-6beta; therapy;  
KW immune system-related disorder; inflammatory disease; immunosuppressive;  
KW bowel disease; encephalitis; atherosclerosis; gastrointestinal-Gen;

KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;  
KW multiple sclerosis; Crohn's disease; autoimmune encephalitis; allergy;  
KW graft versus host disease; GVHD; antiinflammatory; psoriasis; arthritis;  
KW neuroprotective; antiarteriosclerotic; dermatological; asthma; receptor;  
KW gene; ss.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH 25..927  
FT CDS /tag= a  
FT /product= "Human TNFR-6alpha protein"  
FT sig\_peptide 1..114  
FT /tag= b  
FT mat\_peptide 115..924  
FT /tag= c  
FT /product= "Human mature TNFR-6alpha protein"

XX WO200218622-A2.  
XX  
XX 07-MAR-2002.  
XX  
XX 24-AUG-2001; 2001WO-US26396.  
XX  
XX 25-AUG-2000; 2000US-227598P.  
PR 21-NOV-2000; 2000US-252131P.  
PR 06-JUL-2001; 2001US-303224P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Gentz RL, Ebner R, Yu G, Ruben SM, Ni J, Peng P;  
PI  
XX  
XX WPI; 2002-281068/32.  
DR P-PSDB; AAE20848.  
XX  
XX Novel nucleic acid molecules comprising a polynucleotide encoding human  
PT tumor necrosis factor receptor (TNFR)-6alpha and 6beta polypeptides  
PT useful for treating disease e.g. inflammatory and autoimmune disorders  
PT  
XX

XX Example 1; Fig 1; 350pp; English.  
XX  
XX The invention relates to human tumour necrosis factor receptor (TNFR)-  
CC 6alpha and 6beta protein and their corresponding nucleic acids. The  
CC invention provides screening methods for identifying agonists and  
CC antagonists of TNFR-6alpha and 6beta activity. The invention also  
CC provides diagnostic and therapeutic methods for detecting and treating  
CC immune system-related disorders. The method is useful for treating or  
CC preventing an inflammatory disease or disorder selected from bowel  
CC disease, encephalitis, atherosclerosis and psoriasis, an autoimmune  
CC disease or disorder selected from systemic lupus erythematosus,  
CC arthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease,  
CC and autoimmune encephalitis, graft versus host disease (GVHD), and an  
CC allergy or asthma. The present sequence is human TNFR-6alpha cDNA.  
XX

SQ Sequence 1077 BP; 196 A; 360 C; 326 G; 195 T; 0 other;  
Query Match 100.0%; Score 813; DB 24; Length 1077;  
Best Local Similarity 100.0%; Pred. No. 5.1e-145;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCGAAAAACACCCACTTACCCCTGGCGGGAGCGAGACAGAGGAGCGGGTGGTGTC 60  
DB 112 GTGGCGAAAAACACCCACTTACCCCTGGCGGGAGCGAGACAGAGGAGCGGGTGGTGTC 171  
QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGTCAGCGGGCGTGGCCGAGACACGCCACGACG 120  
DB 172 GCCCAGTGGCCCCCAGGACCTTTGTGTCAGCGGGCGTGGCCGAGACACGCCACGACG 231  
QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTTGGAACTACCTGGAGCGCTGCCGC 180  
DB 232 TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTTGGAACTACCTGGAGCGCTGCCGC 291

QY 181 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGACGCGCTTGCACGCCACCCAC 240  
DB 292 TACTGCAACGTCCTCTGCGGGGAGCGTGAGGAGGAGGACGCGCTTGCACGCCACCCAC 351  
QY 241 AACCGTGCCTGCGGCTGCCGACCCGCTTCTTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 300  
DB 352 AACCGTGCCTGCGGCTGCCGACCCGCTTCTTTCGCGCACGCTGGTTTCTGCTTGGAGCAC 411  
QY 301 GCATCGTGTCCACCTGCTGCGGCGTGATGCCCCCGGGACCCCCAGCAGAACACGACG 360  
DB 412 GCATCGTGTCCACCTGCTGCGGCGTGATGCCCCCGGGACCCCCAGCAGAACACGACG 471  
QY 361 TGCAGCGCTGCCCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGCAGAGTCCAG 420  
DB 472 TGCAGCGCTGCCCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGCAGAGTCCAG 531  
QY 421 CCCCACCGCAACTGTCACGCGCCCTGGGCGCTTCAATGTGCGCAGGCTCTTCTCTCCCAT 480  
DB 532 CCCCACCGCAACTGTCACGCGCCCTGGGCGCTTCAATGTGCGCAGGCTCTTCTCTCCCAT 591  
QY 481 GACACCTGTGCAACGCTGCTGCTTCCCGCTCAGCACGAGGTACAGGAGCTGAG 540  
DB 592 GACACCTGTGCAACGCTGCTGCTTCCCGCTCAGCACGAGGTACAGGAGCTGAG 651  
QY 541 GAGTGTGAGCGTGCGCTCATCGACTTTGTGGCTTCCAGGACATCTCCATCAAGAGGCTG 600  
DB 652 GAGTGTGAGCGTGCGCTCATCGACTTTGTGGCTTCCAGGACATCTCCATCAAGAGGCTG 711  
QY 601 CAGCGGCTGCTGCGAGGCGCTCGAGGCGCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 660  
DB 712 CAGCGGCTGCTGCGAGGCGCTCGAGGCGCCCGGAGGGCTGGGGTCCGACACCAAGGGCGGGC 771  
QY 661 CCGCGGCGCTTGCAGCTGAAGCTGCGTGGCGGCTCACCGAGCTCTGTGGGGCGCAGGAC 720  
DB 772 CCGCGGCGCTTGCAGCTGAAGCTGCGTGGCGGCTCACCGAGCTCTGTGGGGCGCAGGAC 831  
QY 721 GGGGCGCTGCTGGTGGCGGCTGCTGAGGCGCTGCGCGTGGCCAGGATGCCCGGCTGGAG 780  
DB 832 GGGGCGCTGCTGGTGGCGGCTGCTGAGGCGCTGCGCGTGGCCAGGATGCCCGGCTGGAG 891  
QY 781 CGGAGCGTCCGTGAGCGCTTCTCTCCCTGTGTCAC 813  
DB 892 CGGAGCGTCCGTGAGCGCTTCTCTCCCTGTGTCAC 924

Search completed: January 6, 2003, 13:55:32  
Job time : 233 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:45:41 ; Search time 1966 Seconds  
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6697.320 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813

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Scoring table: IDENTITY\_NUC

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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EST.\*  
1: em\_estda.\*  
2: em\_esthum.\*  
3: em\_estln.\*  
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7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
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16: em\_estom.\*  
17: gb\_gss.\*  
18: em\_gss\_hum.\*  
19: em\_gss\_inv.\*  
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22: em\_gss\_fun.\*  
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24: em\_gss\_mus.\*  
25: em\_gss\_other.\*  
26: em\_gss\_pro.\*  
27: em\_gss\_rtd.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	ID	Description
1	657	80.8	1118	BI821789 603035863
2	594	73.1	617	BE878908 601492609
3	577.4	71.0	728	BM680786 UI-B-E01-
4	577	70.6	679	BE878006 601489784
5	573.8	70.6	863	BQ687526 AGENCOURT
6	567.2	69.8	572	BM767535 K-EST0050

7	541.8	66.6	1203	13	BM480312	AGENCOURT
8	529	65.1	1037	12	BC679499	BC679499 602627514
9	499.8	61.5	874	12	BF339551	BF339551 602039016
10	482.6	59.4	692	10	AM083241	AM083241 xc07a04.x
11	466.8	57.4	600	10	AM262121	AM262121 xq31d04.x
12	458	56.3	568	14	BQ019285	UI-H-DT1-
13	428.6	52.7	588	13	BI838357	BI838357 603083306
14	421.6	51.9	551	12	BE879166	BE879166 601486906
15	411.6	50.6	540	10	AM471440	AM471440 xw59e06.x
16	405	49.8	606	14	BM767446	BM767446 K-EST0049
17	400.2	49.2	605	14	BM767088	BM767088 K-EST0049
18	400.2	49.2	605	14	BM767418	BM767418 K-EST0049
19	393.8	48.4	616	14	BM743072	BM743072 K-EST0016
20	392.8	48.3	596	14	BM767064	BM767064 K-EST0049
21	389.4	47.9	554	14	AM464298	AM464298 BP230015A
22	388.4	47.8	1216	14	BQ716334	AGENCOURT
23	387.2	47.6	514	10	AM662363	AM662363 h125f01.x
24	387	47.6	588	14	BM756087	BM756087 K-EST0034
25	387	47.6	593	14	BM759026	BM759026 K-EST0038
26	383.8	47.2	486	14	BM831338	BM831338 K-EST0105
27	381.4	46.9	475	9	AI718743	AI718743 aeg5h04.x
28	377	46.4	697	12	BE873766	BE873766 601483915
29	359	44.2	478	12	BF001490	BF001490 7988h10.x
30	354	43.5	515	10	AM083914	AM083914 xc25902.x
31	345.2	42.5	459	10	AM014771	UI-H-B10-
32	339.8	41.8	384	14	BM738195	BM738195 K-EST0002
33	336.4	41.4	448	14	BM672727	UI-F-CO0-
34	324	39.9	445	9	AI857725	AI857725 w121a08.x
35	315.2	38.8	524	14	BM833454	BM833454 K-EST0108
36	311.8	38.4	453	10	AM204959	AM204959 UI-H-B11-
37	308.8	38.0	467	9	AA025673	AA025673 z69h09.s
38	308	37.9	436	9	AI290210	AI290210 q179q12.x
39	305	37.5	452	10	AM771720	AM771720 h171a02.x
40	300	36.9	430	9	AI561219	AI561219 tq27c11.x
41	292.8	36.0	500	14	BM833463	BM833463 K-EST0108
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43	282.4	34.7	340	10	AM16995	xx10e06.x
44	281.8	34.7	417	10	AM06931	AM06931 wt08b06.x
45	280	34.4	405	9	AI520716	AI520716 t106f10.x

## ALIGNMENTS

RESULT 1  
BI821789  
LOCUS 1118 bp mRNA EST 04-OCT-2001  
DEFINITION 603035863F1 NIH\_MGC\_115 Homo sapiens CDNA clone IMAGE:5176910 5',  
mRNA sequence.  
ACCESSION BI821789  
VERSION BI821789.1 GI:15933339  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 1118)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHAM11440 row: n column: 15  
High quality sequence stop: 758.  
Location/Qualifiers  
1. 1118

FEATURES  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5176910"  
/clone\_lib="NIH\_MGC\_115"  
/lab\_host="DH10B"  
/notes="Organ: pooled brain, lung, testis; Vector:  
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."  
BASE COUNT 223 a 377 c 339 g 179 t  
ORIGIN

Query Match 80.8%; Score 657; DB 13; Length 1118;  
Best Local Similarity 99.4%; Pred. No. 2.2e-113;  
Matches 701; Conservative 0; Mismatches 4; Indels 4; Gaps 4;  
QY 110 GCCCCACGAGTGGGCCGCTGTCCACGGCCCACTACAGCGAGTCTTGGAACTACCTGG 169  
Db 1 GCCCCACGAGTGGG-CGCTGTCCACGGCCCACTACAGCGAGTCTTGGAACTACCTGG 59  
QY 170 A-GCGTGGCCGCTACTGCAACGTCCTCTGTGGGGAGCGTGTGAGGAGGAGGACGCGCTTGC 228  
Db 60 AGGCGCTGCCGCTACTGCAACGTCCTCTGTGGGGAGCGTGTGAGGAGGAGGACGCGCTTGC 119  
QY 229 CAGCCACCCACACCGTGTGCTGCGGTGCGGACCGGCTTCTTCGCGCAGCGTGGTTTC 288  
Db 120 CAGCCACCCACACCGTGTGCTGCGGTGCGGACCGGCTTCTTCGCGCAGCGTGGTTTC 179  
QY 289 TGCTTGAGCAGCATCGTGTCCACCTGTGTCGGCGGTGATTTGCCGGGACACCCCGAGC 348  
Db 180 TGCTTGAGCAGCATCGTGTCCACCTGTGTCGGCGGTGAT-TGCCGGGACACCCCGAGC 238  
QY 349 CAGAACACGAGTGCCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGTCA 408  
Db 239 CAGAACACGAGTGCCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGTCA 298  
QY 409 GAGCAGTGCCAGCCACCGCACTGACCGCCCTGGGCGCTGGCCCTCAATGTGCCAGGC 468  
Db 299 GAGCAGTGCCAGCCACCGCACTGACCGCCCTGGGCGCTGGGCGCTCAATGTGCCAGGC 358  
QY 469 TCTTCTCCATGACACCTGTGACCCAGCTGCACTGGCTTCCCGCTCAGCACCAGGGTA 528  
Db 359 TCTTCTCCATGACACCTGTGACCCAGCTGCACTGGCTTCCCGCTCAGCACCAGGTA 417  
QY 529 CCAGGAGCTGAGGAGTGTGAGCGTGCCTGATCGACTTTGTGGCTTTTCCAGGACATCTCC 588  
Db 418 CCAGGAGCTGAGGAGTGTGAGCGTGCCTGATCGACTTTGTGGCTTTTCCAGGACATCTCC 477  
QY 589 ATCAGAGGCTGACGCGGCTGTGACGGCTTCAGCGCCCTCGAGCCCGGAGGCTGGGCTCCGACA 648  
Db 478 ATCAAGAGGCTGACGCGGCTGTGACGGCTTCAGCGCCCTCGAGCCCGGAGGCTGGGCTCCGACA 537  
QY 649 CCAAGGCGGGCCCGCGGCTTTCAGCTGAAGCTGGGTGGGCGGCTCAGCGAGCTCCTG 708  
Db 538 CCAAGGCGGGCCCGCGGCTTTCAGCTGAAGCTGGGTGGGCGGCTCAGCGAGCTCCTG 597  
QY 709 GGGCGCAGGACGGGGCGCTGCTGGTGTGCTGAGCGCTGTGAGCGCTGTGCGGTGGCAGGATG 768  
Db 598 GGGCGCAGGACGGGGCGCTGCTGGTGTGCTGAGCGCTGTGAGCGCTGTGCGGTGGCAGGATG 657  
QY 769 CCGGGCTGGAGCGGAGGCTCCGTGAGGCTTCTCCTCTGTGCAC 813  
Db 658 CCGGGCTGGAGCGGAGGCTCCGTGAGGCTTCTCCTCTGTGCAC 702

LOCUS BE878908 617 bp mRNA linear EST 20-OCT-2000  
DEFINITION 601492609F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3894794 5',  
mRNA sequence.  
ACCESSION BE878908  
VERSION BE878908.1 GI:10327684  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 617)  
NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTF/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLaM9685 row: a column: 03  
High quality sequence stop: 617.  
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Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/tissue\_type="large cell carcinoma, undifferentiated"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."  
BASE COUNT 91 a 224 c 203 g 99 t  
ORIGIN  
Query Match 73.1%; Score 594; DB 12; Length 617;  
Best Local Similarity 99.8%; Pred. No. 1.3e-101;  
Matches 605; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 156 CTGGAACCTACCTGGAGCGTGGCGTACTGCAACGTCCTCTGCGGGAGCGTGAGGAGGA 215  
Db 3 CTGGAACCTACCTGGAGCGTGGCGTACTGCAACGTCCTCTGCGGGAGCGTGAGGAGGA 62  
QY 216 GGCACGGGCTTGCCACGCCACCAACCGTGCCTGCGCGCTGCGCGGCTTCTTCCG 275  
Db 63 GGCACGGGCTTGCCACGCCACCAACCGTGCCTGCGCGCTGCGCGGCTTCTTCCG 122  
QY 276 GCACGCTGGTTCTGTGTTGGAGCACGTCATGTCACCTGTCACCTGGTCCGCGCTGATTCGCC 335  
Db 123 GCACGCTGGTTCTGTGTTGGAGCACGTCATGTCACCTGTCGCGGCTGATTCGCC 182  
QY 336 GGGCACCCCGCAGCAGAACACGAGTGCAGCGCTGCCCGCCCGCAGGACCTTCTCAGCCAG 395  
Db 183 GGGCACCCCGCAGCAGAACACGAGTGCAGCGCTGCCCGCCCGCAGGACCTTCTCAGCCAG 242  
QY 396 CAGCTCCAGCTCAGACAGTGCAGCGCCCGCAGCGCACTGCAGCGCCCTGGGCTTGGCCCT 455  
Db 243 CAGCTCCAGCTCAGACAGTGCAGCGCCCGCAGCGCACTGCAGCGCCCTGGGCTTGGCCCT 302  
QY 456 CAATGTGCAGGCTCTTCTCTCCATGACACCTGTGACACCTGTGACAGCTGACCTGGCTTCCCCCT 515  
Db 303 CAATGTGCAGGCTCTTCTCTCCATGACACCTGTGACAGCTGACCTGGCTTCCCCCT 362  
QY 516 CAGCACCGGTTACAGGAGCTGAGAGTGTGAGCGTGCCTGATCGACTTTGTGCTTT 575  
Db 363 CAGCACCGGTTACAGGAGCTGAGAGTGTGAGCGTGCCTGATCGACTTTGTGCTTT 422  
QY 576 CCAGGACATCTCCATCAAGAGGCTGCAGGGCTGTGTCAGGCGCTTCGAGGCCCCGGAGGG 635

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Db 423 CCAGGACATCTCCATCAAGAGGCTGCGACGCGCTCTCAGGCCCTTCAGAGGCCCGGAGGG 482
Qy 636 CTGGGGTCCGACACCAAGGGGCGGGCGGCGCTTGCAGCTGAAGTGGGTGGGGGCT 695
Db 483 CTGGGGTCCGACACCAAGGGGCGGGCGGCGCTTGCAGCTGAAGTGGGTGGGGGCT 542
Qy 696 CACGAGCTCTCTGGGGGCGGAGACGAGGCGGCGCTGCTGTGCGCTGTGAGCGCTGCG 755
Db 543 CACGAGCTCTCTGGGGGCGGAGACGAGGCGGCGCTGCTGTGCGG-TGCTGACAGGCGCTGCG 601
Qy 756 CGTGGC 761
Db 602 CGTGGC 607

RESULT 3
BM680786 728 bp mRNA linear EST 27-FEB-2002
LOCUS UI-E-BO1-a3c-j-12-0-UI.s1 UI-E-BO1 Homo sapiens cDNA clone
DEFINITION UI-E-BO1-a3c-j-12-0-UI 3', mRNA sequence.
ACCESSION BM680786
VERSION BM680786.1 GI:18990682
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 728)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..728
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/clone_1ib="UI-E-BO1"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/notes="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-BO1 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGGTATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
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|||||
Institute (NEI).
TAG LIB=UI-E-BO1
TAG TISSUE=human fetal eye
TAG_SBO=CGGTATACC"
BASE COUNT 133 a 218 c 248 g 129 t
ORIGIN

Query Match 71.0%; Score 577.4; DB 14; Length 728;
Best Local Similarity 99.3%; Pred. No. 1.7e-98;
Matches 591; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 222 GCGTTGCCAGCGCCACCCACACCGTGTGCGCTGCGCTGCCGACCGGCTTTTGGCGGACG 281
Db 705 GCGTTGCCAGCGCCACCCACACCGTGTGCGCTGCGCTGCCGACCGGCTTTTGGCGGACG 646
Qy 282 TGGTTTCTGCTTGGAGCAGCAGCATGCTGTCCACTGTGCTGCGGCTGATTTGGCGGCGAC 341
Db 645 TGGTTTCTGCTTGGAGCAGCAGCATGCTGTCCACTGTGCTGCGGCTGATTTGGCGGCGAC 586
Qy 342 CCCAGCAGAGACAGCAGCGAGTGCAGCGTGCCTGCCCGGACGACCTTCTCAGCCAGAGCTC 401
Db 585 CCCAGCAGAGACAGCAGCGAGTGCAGCGTGCCTGCCCGGACGACCTTCTCAGCCAGAGCTC 526
Qy 402 CAGCTCAGAGCAGTGCAGCGCCACCGCAACTGACGCGCTGCGCTGCGCTCAATGT 461
Db 525 CAGCTCAGAGCAGTGCAGCGCCACCGCAACTGACGCGCTGCGCTGCGCTCAATGT 466
Qy 462 GCCAGGCTCTTCTCTCCATATACACCTGTGTACACAGCTGACTGTGCTTCCCTCAGGAC 521
Db 465 GCCAGGCTCTTCTCTCCATATACACCTGTGTACACAGCTGACTGTGCTTCCCTCAGGAC 406
Qy 522 CAGGATAC--CAGGAGCTAGAGTGTGTGAGCGTGCCTGATGACTTGTGCTTTCCA 578
Db 405 CAGGATAC--CAGGAGCTAGAGTGTGTGAGCGTGCCTGATGACTTGTGCTTTCCA 346
Qy 579 GGAATCTTCATCAAGAGGCTGCGAGCGCTGTGACAGCCCTTGAGGCCCGGAGGGCTG 638
Db 345 GGAATCTTCATCAAGAGGCTGCGAGCGCTGTGACAGCCCTTGAGGCCCGGAGGGCTG 286
Qy 639 GGGTCCGACACCAAGGGCGGGCGCGGCTTTCAGAGTGAAGTGTGCTGCGCTCAC 698
Db 285 GGGTCCGACACCAAGGGCGGGCGCGGCTTTCAGAGTGAAGTGTGCTGCGCTCAC 226
Qy 699 GGAATCTTCGAGGGCGGAGGACGGGGCGGCTGAGCGGCTCTGAGGCGTGGCGCT 758
Db 225 GGAATCTTCGAGGGCGGAGGACGGGGCGGCTGAGCGGCTCTGAGGCGTGGCGCT 166
Qy 759 GGCCAGGATGCCCGGCGCTGAGCGAGCGTCCGTGAGCGCTTCTCTCTGTGCAC 813
Db 165 GGCCAGGATGCCCGGCGCTGAGCGAGCGTCCGTGAGCGCTTCTCTCTGTGCAC 111

RESULT 4
BE878006 679 bp mRNA linear EST 20-OCT-2000
LOCUS BE878006
DEFINITION 601489784F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5',
mRNA sequence.
ACCESSION BE878006
VERSION BE878006.1 GI:10326782
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 679)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM9677 row: h column: 21  
High quality sequence stop: 672.

## FEATURES

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1. .679  
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/note="Organ: lung; Vector: pCMV-Sport6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.1 kb. Library constructed by Life Technologies."

BASE COUNT 113 a 239 c 204 g 123 t  
ORIGIN

Query Match 71.0%; Score 577; DB 12; Length 679;  
Best Local Similarity 100.0%; Pred. No. 1.9e-98;  
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 11 CCACAACTGCTGCTGCGCTGCGCACCGGCTTCTTGGCGACGCTGTTTCTGCTTGA 70  
QY 297 GCAGCATGCTGCTACCTGCTGCGCGCTGATTGCCCCGGGACCCCGGACGACAC 356  
Db 71 GCAGCATGCTGCTACCTGCTGCGCGCTGATTGCCCCGGGACCCCGGACGACAC 130  
QY 357 GCAGTGCAGCGCTGCCCCCGGACGCTTCTCAGCGAGCAGCTCCAGCTCAGAGCAGTG 416  
Db 131 GCAGTGCAGCGCTGCCCCCGGACGCTTCTCAGCGAGCAGCTCCAGCTCAGAGCAGTG 190  
QY 417 CAGCCCCACGCAACTGACGCGGCTTGGGCTGGGCTGAGCTCAATGTGCGAGGCTTCTCTC 476  
Db 191 CAGCCCCACGCAACTGACGCGGCTTGGGCTGGGCTGAGCTCAATGTGCGAGGCTTCTCTC 250  
QY 477 CCATGACACCTGTGACACGAGCTGCACTGGCTTCCCTCAGACACGAGGTACAGAGC 536  
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QY 537 TGAGGAGTGTGAGCGTGCCTGCTATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAG 596  
Db 311 TGAGGAGTGTGAGCGTGCCTGCTATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAG 370  
QY 597 GCTGACGCGCTGTGACGCGCTTGAAGCCCGGAGGCTGGGCTCCGACACCAAGGGC 656  
Db 371 GCTGACGCGCTGTGACGCGCTTGAAGCCCGGAGGCTGGGCTCCGACACCAAGGGC 430  
QY 657 GGGCGGCGGCTTGCAGCTGAGCTGCGTCCGCGGCTCAGCGAGCTCTCGGGGCGCA 716  
Db 431 GGGCGGCGGCTTGCAGCTGAGCTGCGTCCGCGGCTCAGCGAGCTCTCGGGGCGCA 490  
QY 717 GGACGGGGCGCTGTGCTGGGCTGTGCTGACGGCGCTCGCGCTGGCCAGGATGCCGGGCT 776  
Db 491 GGACGGGGCGCTGTGCTGGGCTGTGCTGACGGCGCTCGCGCTGGCCAGGATGCCGGGCT 550  
QY 777 GGACGGAGCGCTGCTGAGCGCTTCTCTCTCTGTCAC 813  
Db 551 GGACGGAGCGCTGCTGAGCGCTTCTCTCTCTGTCAC 587

RESULT 5  
BQ687526  
LOCUS BQ687526 863 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8345883 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250691  
5', mRNA sequence.  
ACCESSION BQ687526  
VERSION BQ687526.1 GI:21812842

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 863)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM2394 row: c column: 12  
High quality sequence stop: 599.  
Location/Qualifiers  
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/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
Note: this is a NIH\_MGC Library."  
BASE COUNT 133 a 312 c 276 g 141 t 1 others  
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Query Match 70.6%; Score 573.8; DB 14; Length 863;  
Best Local Similarity 94.8%; Pred. No. 8e-98;  
Matches 637; Conservative 0; Mismatches 28; Indels 7; Gaps 4;  
QY 1 GTGGCAGAAACACCCACCTTACCTCCCTGGGGGACGACAGACAGGGAGCGGCTGGTGTGC 60  
Db 149 GTGGCAGAAACACCCACCTTACCTCCCTGGGGGACGACAGACAGGGAGCGGCTGGTGTGT 208  
QY 61 GCCCAGTGCCTCCAGGACCTTTGTGACGCGCGCTGCGCGGACAGACAGCCCGGACGACG 120  
Db 209 GCCCAGTGCCTCCAGGACCTTTGTGACGCGCGCTGCGCGGACAGACAGCCCGGACGACG 268  
QY 121 TGTGGCCCGTGTCTCCACGCGCCACTACACGACGTTCTCGAACTTACCTGGAGCGCTGCCGC 180  
Db 269 TGTGGCCCGTGTCTCCACGCGCCACTACACGACGTTCTGAACTTACCTGGAGCGCTGCCGC 328  
QY 181 TACTGCAACGCTCTCTTGTGCGGGAGCGTGTGAGGAGGACGCGGCTTGCACGCGCCAC 240  
Db 329 TACTGCAACGCTCTCTTGTGCGGGAGCGTGTGAGGAGGACGCGGCTTGCACGCGCCAC 388  
QY 241 AACCGTGCCTGCGCTGCGGACCGGCTTCTTGTGCGGACGCTGGTTCCTTGTGGAGCAC 300  
Db 389 AACCGTGCCTGCGCTGCGGACCGGCTTCTTGTGCGGACGCTGGTTCCTTGTGGAGCAC 448  
QY 301 GCATCGTGTCCACCTGGTGTCCGCGGTGATTGCCCCGGGACCCCGGACGACGACGACG 360  
Db 449 GCATCGTGTCCACCTGGTGTCCGCGGTGATTGCCCCGGGACCCCGGACGACGACGACG 508  
QY 361 TGCCAGCGGTGCCCCCGGACGACCTTCTCAGCGACGAGTCTCCAGCTCAGAGCAGTGCAG 420  
Db 509 TGCCAGCGGTGCCCCCGGACGACCTTCTCAGCGACGAGTCTCCAGCTCAGAGCAGTGCAG 568  
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Db 569 CCCACCGCACTGACAGCAGCCCTGGGCTTGGGCTTCAATGTCAGAGCTTTCTCTCC 628
Qy 479 ATGACACCCCTGTGCACAGCTGCACTGCTTCCCTCCAGACACAGGATACAGAA--GC 536
Db 629 ATGACAGCTGTGCACAGCTGCACTGCTTCCCTCCAGACACAGGATACAGAAAGCT 688
Qy 537 TGAGAGTGTGACGCTGCTGCTCATGAC-TTGTGCTTTCCAGACATCTCATCAAGA 595
Db 689 GAGGAAGTGTGACGCTGCTGCTCATGACCTTTGTGCTTTCCAGACATCTCATCAAGA 748
Qy 596 GGTGTGAGCGGCTGTGCAGAGCCCTCGAGGCCCGGA--GGGCTGGGTCCGACACCAAG 653
Db 749 AGTGTGAGCGGCTGTGCAGAGCCCTCGAGGCCCGGAAGGCTGGGGGTCCGAAACCA 808
Qy 654 GCGGCGCGCGCGC 665
Db 809 GGGCGCGCGCGC 820

RESULT 6
LOCUS BM767535 572 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0050015 S1SNUS52 Homo sapiens cDNA clone S1SNUS52-3-B03 5',
ACCESSION BM767535
VERSION BM767535.1 GI:19097150
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 572)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: Yongsung@mail.kribb.re.kr
Plate: 3 row: E column: 03
High quality sequence stop: 572.
Location/Qualifiers
1..572
/organism="Homo sapiens"
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/cell_type="Lymphoblast-like"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pCNS; Site: 1; EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tabacco acid pyrophosphatase (TAP). The deapped
intact RNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and

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sequencing about 2,000 ~ 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and Nid14 as 3' primer. The PCR
products were used as template for synthesis of
biotinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin-gel. After removing
DNA-RNA hybrids by centrifuge, the subtracted cDNA
libraries were constructed by transformation of the
remaining DNA into competent cells E. coli Top10F with
electroporation method."

BASE COUNT 90 a 213 c 174 g 95 t
ORIGIN

Query Match 69.8%; Score 567.2; DB 14; Length 572;
Best Local Similarity 99.5%; Pred. No. 1.3e-96;
Matches 569; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 117 GACGTGTGGCCCGTGTCCACCGGCGCACTACACGCACTTCTGGAATCTAGAGGCTG 176
Db 1 GACGTGTGGCCCGTGTCCACCGGCGCACTACACGCACTTCTGGAATCTAGAGGCTG 60
Qy 177 CCGCTACTGCACACGCTCTCTGCGGGAGCGGTGAGAGAGCAGCGGCTTGCCACGCCAC 236
Db 61 CCGCTACTGCACACGCTCTCTGCGGGAGCGGTGAGAGAGCAGCGGCTTGCCACGCCAC 120
Qy 237 CCACAAACGCTGCTGCTGCTGCGGACCGGCTTTCTTGCGGACAGCTGTGTTCTTGGGA 296
Db 121 CCACAAACGCTGCTGCTGCTGCGGACCGGCTTTCTTGCGGACAGCTGTGTTCTTGGGA 180
Qy 297 GCAAGCATGTGTGCCACCTGTGTGCGGGGAGTGTGCGGGGACCCGACAGCAACAC 356
Db 181 GCAAGCATGTGTGCCACCTGTGTGCGGGGAGTGTGCGGGGACCCGACAGCAACAC 240
Qy 357 GCAGTGTCCAGCGGTGCGGCCCCCAAGCACTTCTCAGCCAGCAGCTCAGTCAAGAGAGT 416
Db 241 GCAGTGTCCAGCGGTGCGGCCCCCAAGCACTTCTCAGCCAGCAGTCAAGAGAGT 300
Qy 417 CCAGCCCAACCGCACTGCAAGCGGCTGTGGGCTTGACCAATGTGCCAGGCTTTCTTC 476
Db 301 CCAGCCCAACCGCACTGCAAGCGGCTGTGGGCTTGACCAATGTGCCAGGCTTTCTTC 360
Qy 477 CCATGACACCTGTGTGACACGCTGCACTGCTTCCCTCCAGACACAGGATACAGAGAG 536
Db 361 CCATGACACCTGTGTGACACGCTGCACTGCTTCCCTCCAGACACAGGATACAGAGAG 420
Qy 537 TGAGAGTGTGACGCTGCGGTGATGCACTTGTGTGCTTCCAGACATCTCCATCAAGAG 596
Db 421 TGAGAGTGTGACGCTGCGGTGATGCACTTGTGTGCTTCCAGACATCTCCATCAAGAG 480
Qy 597 GCTGACGCGGCTGTGACAGGCTTCGAGGCCCCGAGAGGCTGGGGTCCGACCAAGGCG 656
Db 481 GCTGACGCGGCTGTGACAGGCTTCGAGGCCCCGAGAGGCTGGGGTCCGACCAAGGCG 540
Qy 657 GGGCGCGCGGCGCTTGCACTGCACTGAAGTGCCTC 688
Db 541 GGGCGCGCGGCGCTTGCACTGCACTGAAGTGCCTC 572

RESULT 7
LOCUS BM480312 1203 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6424187 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491790
ACCESSION BM480312
VERSION BM480312.1 GI:18529354
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```



QY 301 GCATGTCCTCACCCTGTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 360  
Db 494 GCATGTCCTCACCCTGTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 553  
QY 361 TGCACGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 420  
Db 554 TGCACGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 613  
QY 421 CCCCACGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 480  
Db 614 CCCCACGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 672  
QY 481 GACACCTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 538  
Db 673 GACACCTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 732  
QY 539 AGGAGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 588  
Db 733 AGGAGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 792  
QY 589 ATCAAGAGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 645  
Db 793 ATCAAGAGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 852  
QY 646 ACAACGAGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 705  
Db 853 ACAACGAGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 912  
QY 706 CTGGGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 765  
Db 913 CTGGGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 970  
QY 766 ATGCGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 808  
Db 971 --ATGCGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 1011

RESULT 9  
BF339551 874 bp mRNA linear EST 22-NOV-2000  
LOCUS BF339551  
DEFINITION 602039016F1 NCI\_CGAP\_Brn64 Homo sapiens cDNA clone IMAGE:418695  
5', mRNA sequence.  
ACCESSION BF339551  
KEYWORDS BF339551.1 GI:11286006  
SOURCE EST.  
ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 874)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: csapbs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LHM9508 row: p column: 04  
High quality sequence stop: 701.  
Location/Qualifiers

FEATURES  
Source  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4186955"  
/clone\_lib="NCI\_CGAP\_Brn64"  
/issue\_type="glioblastoma with EGFR amplification"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NCI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.57 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

Query Match 61.5%; Score 499.8; DB 12; Length 874;  
Best Local Similarity 87.8%; Pred. No. 5,7e-84;  
Matches 568; Conservative 0; Mismatches 77; Indels 2; Gaps 2;

BASE COUNT 129 a 299 c 301 g 145 t  
ORIGIN  
QY 1 GTGGCAGAAACACCCACTTACCTTGGCGGAGCAGACAGAGGAGCGGCTGTGTGC 60  
Db 185 GTGGCAGAAACACCCACTTACCTTGGCGGAGCAGACAGAGGAGCGGCTGTGTGC 244  
QY 61 GCCAGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 120  
Db 245 GCCAGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 304  
QY 121 TGTGGCCGTCGTCACCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 180  
Db 305 TGTGGCCGTCGTCACCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 364  
QY 181 TACTGCAAGTCTCTGTCGCGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
Db 365 TACTGCAAGTCTCTGTCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424  
QY 241 AACCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 300  
Db 425 AACCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 484  
QY 301 GCATGTCCTCACCCTGTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 360  
Db 485 GCATGTCCTCACCCTGTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 544  
QY 361 TGCACGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 420  
Db 545 TGCACGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 604  
QY 421 CCCCACGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 480  
Db 605 CCCCACGCGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 663  
QY 481 GACACCTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 540  
Db 664 GACACCTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 722  
QY 541 GAGTGTGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 600  
Db 723 AAGTGTGAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 782  
QY 601 CAGCGGCTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 647  
Db 783 GCGGTGTGTCCTGTCGCGGCGTATGTCCTCCCGGACACCCCGACAGACACGACG 829

RESULT 10  
AM083241/c 692 bp mRNA linear EST 14-OCT-1999  
LOCUS AM083241/c  
DEFINITION xc07a04.x1 NCI CGAP Co21 Homo sapiens cDNA clone IMAGE:2583534 3'  
similar to TR\_095407 O95407 DECOY RECEPTOR 3. :contains 11.b1 MER22  
repetitive element ;, mRNA sequence.

ACCESSION AM083241  
KEYWORDS AM083241.1 GI:6038393  
VERSION EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 692)  
NIH-MGC http://www.ncbi.nlm.nih.gov/ncicgap/  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40UP from Gibco  
High quality sequence stop: 414.

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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Normalized to Cot >500. Average insert size 1.04kb.  
Normalized version of NCI\_CGAP\_Co18. Library constructed by Life Technologies."  
BASE COUNT 136 a 205 c 235 g 115 t 1 others

Query Match 59.4%; Score 482.6; DB 10; Length 692;  
Best Local Similarity 97.7%; Pred. No. 9.1e-81;  
Matches 510; Conservative 0; Mismatches 10; Indels 2; Gaps 2;  
QY 293 TGGAGCAGCATCGTTCACCTGGTGGCGGTGATGTCGCCGGGACCCCGGCGAGA 352  
Db 619 TGGAGCAGCATCGTTCACCT-GTCCGGGTGATGTCGCCGGGACCCCGGCGAGA 561  
QY 353 ACAGGAGTCCAGCGTGGCCCCCAGGACCTTCTCAGCAGCAGCTCCAGCTCAGC 412  
Db 560 ACAGCAGTCCAGCGTGGCCCCCAGGACCTTCTCAGCAGCAGCTCCAGCTCAGC 501  
QY 413 AGTGCCAGCCCGGCACTGCAGCGCCCTGGGCCCTCAATGTGCCAGGCTCTT 472  
Db 500 AGTGCCAGCCCGGCACTGCAGCGCCCTGGGCCCTCAATGTGCCAGGCTCTT 441  
QY 473 CTCTCCATGACACCTGTGCACAGCTGCATCGACTTTGGGCTTCCAGGACATCTCCATCA 532  
Db 440 CTCTCCATGACACCTGTGCACAGCTGCATCGACTTTGGGCTTCCAGGACATCTCCATCA 381  
QY 533 GAGCTGAGGAGTGAGCGTGGCGTATCGACTTTGGGCTTCCAGGACATCTCCATCA 592  
Db 380 GAGCTGAGGAGTGAGCGTGGCGTATCGACTTTGGGCTTCCAGGACATCTCCATCA 321  
QY 593 AGAGGCTGACGCGCTCTCTCAGCGCTTCAGGCGCCCGGAGGCTGGGGTCCGACACAA 652  
Db 320 AGAGGCTGACGCGCTCTCTCAGCGCTTCAGGCGCCCGGAGGCTGGGGTCCGACACAA 261  
QY 653 GGGCGGCGCGGGCGCTTTCAGCTGAAGC-TGCGTCCGGCGGCTTCAGGAGCTCTTGGGG 711  
Db 260 GGGCGGCGCGGGCGCTTTCAGCTGAAGC-TGCGTCCGGCGGCTTCAGGAGCTCTTGGGG 201  
QY 712 GCGCAGACGGGGCGCTGCTGGTGGCGCTGCTGAGCGCTGCGCGTGGCGGAGATGCC 771  
Db 200 GCGCAGACGGGGCGCTGCTGGTGGCGCTGCTGAGCGCTGCGCGTGGCGGAGATGCC 141  
QY 772 GGGCTGAGCGGAGCGTCCGTGAGCGCTTCTCTCCCTGTGCAC 813  
Db 140 GGGCTGAGCGGAGCGTCCGTGAGCGCTTCTCTCCCTGTGCAC 99

RESULT 11  
AW262121/c 600 bp mRNA linear EST 28-DEC-1999  
LOCUS AW262121  
DEFINITION xq31a04.x1 NCI\_CGAP\_Lu28 Homo sapiens cDNA clone IMAGE:2752231.3

similar to TR:095407 095407 DCOY RECEPTOR 3. ; contains TAR1.b1  
TAR1 repetitive element ; mRNA sequence.  
ACCESSION AW262121 GI:6638937  
VERSION AW262121.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 600)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco  
High quality sequence stop: 410.  
FEATURES  
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1. .600  
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/clone="IMAGE:2752231"  
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/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies."  
BASE COUNT 120 a 177 c 199 g 102 t 2 others

Query Match 57.4%; Score 466.8; DB 10; Length 600;  
Best Local Similarity 98.1%; Pred. No. 8.1e-78;  
Matches 471; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
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Db 600 CCGGGCAGCCCGGCGAGTCCAGCGAGTCCAGCGCGTCCCGCCAGGCGACCTTCTCAGCC 541  
QY 394 AGCAGCTCAGGCTCAGAGGAGTCCAGCGCGCCCGGCAACTGCAACGCCCTTGGGCTGGCC 453  
Db 540 AGCAGCTCAGGCTCAGAGGAGTCCAGCGCGCCCGGCAACTGCAACGCCCTTGGGCTGGCC 481  
QY 454 CTCAATGTCCAGGCTTCTCTCCCATGACCCCTGTGACAGCTGACAGCTGCGCTTCCCC 513  
Db 480 CTCAATGTCCAGGCTTCTCTCTCCCATGACCCCTGTGACAGCTGACAGCTGCGCTTCCCC 421  
QY 514 CTCAGCACAGGCTACAGGAGTGTAGAGGTGTAGCGTGTGCGTTCATCGACTTTGTGGCT 573  
Db 420 CTCAGCACAGGCTACAGGAGTGTAGAGGTGTAGCGTGTGCGTTCATCGACTTTGTGGCT 361  
QY 574 TTCCAGGACATCTCCATCAAGAGGCTGACGCGGCTGCTCAGGCCCTCGAGGCCCGCGAG 633  
Db 360 TTCCAGGACATCTCCATCAAGAGGCTGACGCGGCTGCTCAGGCCCTCGAGGCCCGCGAG 301  
QY 634 GGCTGGGTCCGACACAGAGGGGGCGCGCGGCTTTCAGCTGAGCTGCGTCCGCGG 693  
Db 300 GGCTGGGTCCGACACAGAGGGGGCGCGCGGCTTTCAGCTGAGCTGCGTCCGCGG 241  
QY 694 CTCACGAGCTCTCTGGGGCGGAGGACGGGGCGCTCTCTGTGGGCTGTGTGACGGGCTG 753  
Db 240 CTCACGAGCTCTCTGGGGCGGAGGACGGGGCGCTCTCTGTGGGCTGTGTGACGGGCTG 181



Oy	754	CGCGGAGCAGGATCCCGGCCTGGAGCGGACCGTCCGTTCCTCGGTGCAC	813
Db	180	CGCGTGCCAGAGATCCCCGGGCTGGAGCGGACGTTCCGTGAACGCTTCTCCCTGTGCAC	121
RESULT 12			
BQ019285/c			
LOCUS			
DEFINITION	B0019285	568 bp	mRNA linear EST 17-JUN-2002
ACCESSION	U1-H-DTI-awn-1-19-0-U.s1	NCI CGAP_DTI	Homo sapiens CDNA clone
VERSION	IMAGE:5891874.3,		mRNA sequence.
KEYWORDS	B0019285		
SOURCE	B0019285.1	GI:19754562	EST.
ORGANISM	human.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 568)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapds-remail.nih.gov		
	Tissue Procurement: Dr. Jose Mercuende		
	CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa		
	CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: Clone distribution information can be found		
	through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov		
	Seq primer: M13 FORWARD		
	POLYA=Yes.		

FEATURES	
source	Location/Qualifiers
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	/clone_1lb="NCI CGAP DT1"
	/tissue_type="Metastatic Chondrosarcoma"
	/dev_stage="Adult"
	/lab_host="DH10B (Life Technologies)"
	/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP DT1 is a normalized cDNA library containing the following tissue(s): Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTTCCG.
	TAG_L1b=U1-H-DT1
	TAG_TISSUE=lung metastatic chondrosarcoma
	TAG_SEQ=AACTGTTCCG"
BASE COUNT	106 a 170 c 187 g 105 t
ORIGIN	
Query Match	56.3%; Score 458; DB 14; Length 568;
Best Local Similarity	100.0%; Pred. No. 3.6e-76;
Matches 458;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	356 CGCAGTGCAGGCGCGTGCCTTTCAGGCAGCAGCAGCTTCAGAGCAGT 415
DB	568 CGCAGTGCAGGCGCGTGCCTTTCAGGCAGCAGCAGCTTCAGAGCAGT 509
QY	416 GCGAGCCCGCAGCAGCAGCGGCGTGGCGTGGCCCTCAATGTCAGGCTTTTCT 475
DB	508 GCGAGCCCGCAGCAGCAGCGGCGTGGCGTGGCCCTCAATGTCAGGCTTTTCT 449

QY	476	CCCATGACACCCCTTGACACCAAGCTGCATATGGCTTCCCTCCAGACACCAAGGGTACCAAGAG	535
Db	448	CCCATGACACCCCTTGACACCAAGCTGCATATGGCTTCCCTCCAGACACCAAGGGTACCAAGAG	389
QY	536	CTGAGAGATGTGAGCGTGGCCGTCATCGACTTTGTGTGGCTTTCCAGAGACATCTTCATCAAGA	595
Db	388	CTGAGAGATGTGAGCGTGGCCGTCATCGACTTTGTGTGGCTTTCCAGAGACATCTTCATCAAGA	329
QY	596	GGCTGACAGCGGCTGCTGACAGGCCCTTCGAGGCCCGCGAGAGGCTGGGGTCCGACCCAGAGG	655
Db	328	GGCTGACAGCGGCTGCTGACAGGCCCTTCGAGGCCCGCGAGAGGCTGGGGTCCGACCCAGAGG	269
QY	656	CGGGCCGCGCGGCGCTTGTGAGCTGTAAGCTGTGGCGGCTCAAGAGCTCCTGGGGGGCGC	715
Db	268	CGGGCCGCGCGGCGCTTGTGAGCTGTAAGCTGTGGCGGCTCAAGAGCTCCTGGGGGGCGC	209
QY	716	AGGACGGGGGCGCTGTGGTGGCGGCTGCAGAGGCGTGCGGGTGGCCAGAGATGCCCCGGGC	775
Db	208	AGGACGGGGGCGCTGTGGTGGCGGCTGCAGAGGCGTGCGGGTGGCCAGAGATGCCCCGGGC	149
QY	776	TGGAGCGGAGCGTCCGTGAGCGCTTCCCTCGTGAC	813
Db	148	TGGAGCGGAGCGTCCGTGAGCGCTTCCCTCGTGAC	111

RESULT	13
LOCUS	B1838357
DEFINITION	B1838357 588 bp mRNA linear EST 04-OCT-2001
ACCESSION	6030893306F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5222545 5',
VERSION	mRNA sequence.
KEYWORDS	B1838357 GI:15949907
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryote; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL	N1 (bases 1 to 588)
COMMENT	NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapsf@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.lnl.gov Plate: LMNL1559 row: 1 column: 02 High quality sequence stop: 588. Location/Qualifiers 1..588 /organism="Homo sapiens" /db_xref="taxon:9606" /cclone="IMAGE:5222545" /cclone_1lb="NIH_MGC_120" /lab host="DH10B" /note="Organ: pooled pancreas and spleen; Vector: PCMV-SPOrt6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC library."
BASE COUNT	97 a 224 c 171 g 95 t 1 others
ORIGIN	
Query Match	52.7%; Score 428.6; DB 13; Length 588;





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GenCore version 5.1.3  
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OM nucleic - nucleic search, using SW model

Run on: January 6, 2003, 13:48:11 ; Search time 54 Seconds  
(without alignments)  
4617.189 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813  
Sequence: 1 gtcgcagaacaccaccacta.....agcgtctctccctgtgcac 813

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Issued Patents NA: \*  
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2: /cgn2\_6/prodata/2/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/6A COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/PCITUS COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/backtitles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	100.0	1164	2	US-08-794-796-1
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3	533.4	65.6	1859	4	US-09-286-529-19
4	459	56.5	459	4	US-09-286-529-7
5	129.6	15.9	525	3	US-08-997-918-47
6	112	13.8	2432	3	US-08-974-022-1
7	112	13.8	2432	4	US-08-795-445A-1
8	112	13.8	2432	4	US-08-795-447A-1
9	112	13.8	2432	4	US-08-974-186-1
10	112	13.8	2432	4	US-08-795-446B-1
11	112	13.8	2432	4	US-08-706-945D-123
12	110.4	13.6	1324	4	US-08-974-022-3
13	110.4	13.6	1324	4	US-08-795-445A-3
14	110.4	13.6	1324	4	US-08-795-447A-3
15	110.4	13.6	1324	4	US-08-974-186-3
16	110.4	13.6	1324	4	US-08-795-446B-3
17	110.4	13.6	1324	4	US-08-706-945D-125
18	103	12.7	1355	3	US-08-974-022-5
19	103	12.7	1355	4	US-08-795-445A-5
20	103	12.7	1355	4	US-08-795-447A-5
21	103	12.7	1355	4	US-08-974-186-5
22	103	12.7	1355	4	US-08-795-446B-5
23	103	12.7	1355	4	US-08-706-945D-127
24	76	9.3	3331	4	US-09-042-785A-1
25	68	8.4	759	4	US-09-042-785A-6
26	68	8.4	1815	4	US-09-042-785A-24
27	68	8.4	2186	3	US-08-959-382-1

28	68	8.4	2612	4	US-09-042-785A-3	Sequence 3, Appl1
29	68	8.4	2638	4	US-09-042-785A-22	Sequence 22, Appl1
30	68	8.4	3474	4	US-09-527-236A-1	Sequence 1, Appl1
31	56.4	6.9	1719	4	US-09-042-785A-5	Sequence 5, Appl1
32	54.8	6.7	1164	4	US-08-794-796-1	Sequence 1, Appl1
33	54.8	6.7	1347	4	US-09-286-529-18	Sequence 18, Appl1
34	52	6.4	2793	1	US-08-209-747-1	Sequence 1, Appl1
35	52	6.4	2793	1	US-08-458-298-1	Sequence 1, Appl1
36	51.6	6.3	3796	2	US-08-762-308-11	Sequence 11, Appl1
37	51.6	6.3	3796	2	US-09-844-634-10	Sequence 10, Appl1
38	51.6	6.3	3813	2	US-08-650-000-3	Sequence 3, Appl1
39	51.6	6.3	3813	6	5395760-3	Patent No. 5395760
40	49.6	6.1	691	1	US-08-266-080B-12	Sequence 12, Appl1
41	49.6	6.1	691	5	PCT-US95-05423-12	Sequence 12, Appl1
42	49.6	6.1	705	4	US-09-326-394-3	Sequence 3, Appl1
43	48.6	6.1	8906	2	US-08-826-267-1	Sequence 1, Appl1
44	48.6	6.0	1878	3	US-08-966-139-14	Sequence 14, Appl1
45	48.6	6.0	1878	4	US-08-995-659-14	Sequence 14, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-794-796-1  
; Sequence 1, Application US/08794796  
; Patent No. 5885800  
GENERAL INFORMATION:  
; APPLICANT: Emery, John  
; APPLICANT: Tan, KB  
; APPLICANT: Truneh, Alem  
; APPLICANT: Young, Peter  
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,  
; TITLE OF INVENTION: TR4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road  
; City: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/794, 796  
; FILING DATE: 04-FEB-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Han, William T  
; REFERENCE/DOCKET NUMBER: 34,344  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4026  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1164 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-794-796-1  
Query Match 100.0%; Score 813; DB 2; Length 1164;  
Best Local Similarity 100.0%; Pred. No. 2.6e-154;

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Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGGAGCGGCTGGTGTGC 60
Db 198 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGGAGCGGCTGGTGTGC 257
QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGGTGCGCGGAGACAGCCCCACGACG 120
Db 258 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGGTGCGCGGAGACAGCCCCACGACG 317
QY 121 TGTGGGCGCGTGTACACGCGGCCACTACACGACGTTCTGGAACCTACCTGGAGCGCTGCCGC 180
Db 318 TGTGGGCGCGTGTACACGCGGCCACTACACGACGTTCTGGAACCTACCTGGAGCGCTGCCGC 377
QY 181 TACTGCAACGTCCTCTGCGGGAGCGTGTAGGAGGAGGACAGGCGCTTGCACGCGCACCCAC 240
Db 378 TACTGCAACGTCCTCTGCGGGAGCGTGTAGGAGGAGGACAGGCGCTTGCACGCGCACCCAC 437
QY 241 AACCGTGCCTGCGCGTGCACGCGGCTTCTTCCGCGACGCTGGTTTCTGCTTGGAGCAC 300
Db 438 AACCGTGCCTGCGCGTGCACGCGGCTTCTTCCGCGACGCTGGTTTCTGCTTGGAGCAC 497
QY 301 GCATCGTGTCCACCTGTGCGCGCGTGAATTGCCCGCGGACACCCCGGACAGCAACGCGAG 360
Db 498 GCATCGTGTCCACCTGTGCGCGCGTGAATTGCCCGCGGACACCCCGGACAGCAACGCGAG 557
QY 361 TGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGGAGCTCCAGCTCAGAGAGTGCCAG 420
Db 558 TGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGGAGCTCCAGCTCAGAGAGTGCCAG 617
QY 421 CCCACCGCAACTGCAGCGGCGCTGGGCGCTCAATGTGCCAGGCTCTTCTCCCAT 480
Db 618 CCCACCGCAACTGCAGCGGCGCTGGGCGCTCAATGTGCCAGGCTCTTCTCCCAT 677
QY 481 GACACCTGTGCACAGCTGCATGTGCTTCCCGCTCAGCACAGGCTACAGGAGCTGAG 540
Db 678 GACACCTGTGCACAGCTGCATGTGCTTCCCGCTCAGCACAGGCTACAGGAGCTGAG 737
QY 541 GAGTGTAGCGTCCGCTATCGACTTTGTGGCTTTCAGAGACATCTCCATCAAGAGGCTG 600
Db 738 GAGTGTAGCGTCCGCTATCGACTTTGTGGCTTTCAGAGACATCTCCATCAAGAGGCTG 797
QY 601 CAGCGGCTGTGCAGCGCTCAGGCGCCCGGAGGCTGGGGTCCGACACCAAGGGCGGC 660
Db 798 CAGCGGCTGTGCAGCGCTCAGGCGCCCGGAGGCTGGGGTCCGACACCAAGGGCGGC 857
QY 661 CGCGCGGCTTGCAGCTGAAGCTGCGCTCGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 720
Db 858 CGCGCGGCTTGCAGCTGAAGCTGCGCTCGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 917
QY 721 GGGGCGCTGTGTGGGCTGTGCGAGGCGCTGCGGCTGCGCAGGATGCCCGGCTGGAG 780
Db 918 GGGGCGCTGTGTGGGCTGTGCGAGGCGCTGCGGCTGCGCAGGATGCCCGGCTGGAG 977
QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813
Db 978 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 1010
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RESULT 2

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US-09-286-529-18
; Sequence 18, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1347
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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-18
Query Match 100.0%; Score 813; DB 4; Length 1347;
Best Local Similarity 100.0%; Pred. No. 2.6e-154;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGGAGCGGCTGGTGTGC 60
Db 405 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGGAGCGGCTGGTGTGC 464
QY 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGGTGCGCGGAGACAGCCCCACGACG 120
Db 465 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGGTGCGCGGAGACAGCCCCACGACG 524
QY 121 TGTGGGCGCGTGTACACGCGGCCACTACACGACGTTCTGGAACCTACCTGGAGCGCTGCCGC 180
Db 525 TGTGGGCGCGTGTACACGCGGCCACTACACGACGTTCTGGAACCTACCTGGAGCGCTGCCGC 584
QY 181 TACTGCAACGTCCTCTGCGGGAGCGTGTAGGAGGAGGACAGGCGCTTGCACGCGCACCCAC 240
Db 585 TACTGCAACGTCCTCTGCGGGAGCGTGTAGGAGGAGGACAGGCGCTTGCACGCGCACCCAC 644
QY 241 AACCGTGCCTGCGCGTGCACGCGGCTTCTTCCGCGACGCTGGTTTCTGCTTGGAGCAC 300
Db 645 AACCGTGCCTGCGCGTGCACGCGGCTTCTTCCGCGACGCTGGTTTCTGCTTGGAGCAC 704
QY 301 GCATCGTGTCCACCTGTGCGCGCGTGAATTGCCCGCGGACACCCCGGACAGCAACGCGAG 360
Db 705 GCATCGTGTCCACCTGTGCGCGCGTGAATTGCCCGGACAGCAACGCGAG 764
QY 361 TGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGGAGCTCCAGCTCAGAGAGTGCCAG 420
Db 765 TGCAGCGTGGCCCCCAGGACCTTCTCAGCCAGGAGCTCCAGCTCAGAGAGTGCCAG 824
QY 421 CCCACCGCAACTGCAGCGGCGCTGGGCGCTCAATGTGCCAGGCTCTTCTCCCAT 480
Db 825 CCCACCGCAACTGCAGCGGCGCTGGGCGCTCAATGTGCCAGGCTCTTCTCCCAT 884
QY 481 GACACCTGTGCACAGCTGCATGTGCTTCCCGCTCAGCACAGGCTACAGGAGCTGAG 540
Db 885 GACACCTGTGCACAGCTGCATGTGCTTCCCGCTCAGCACAGGCTACAGGAGCTGAG 944
QY 541 GAGTGTAGCGTCCGCTATCGACTTTGTGGCTTTCAGAGACATCTCCATCAAGAGGCTG 600
Db 945 GAGTGTAGCGTCCGCTATCGACTTTGTGGCTTTCAGAGACATCTCCATCAAGAGGCTG 1004
QY 601 CAGCGGCTGTGCAGCGCTCAGGCGCCCGGAGGCTGGGGTCCGACACCAAGGGCGGC 660
Db 1005 CAGCGGCTGTGCAGCGCTCAGGCGCCCGGAGGCTGGGGTCCGACACCAAGGGCGGC 1064
QY 661 CGCGCGGCTTGCAGCTGAAGCTGCGCTCGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 720
Db 1065 CGCGCGGCTTGCAGCTGAAGCTGCGCTCGCGGCTCAGCGAGCTCCTGGGGGCGCAGGAC 1124
QY 721 GGGGCGCTGTGTGGGCTGTGCGAGGCGCTGCGGCTGCGCAGGATGCCCGGCTGGAG 780
Db 1125 GGGGCGCTGTGTGGGCTGTGCGAGGCGCTGCGGCTGCGCAGGATGCCCGGCTGGAG 1184
QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813
Db 1185 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 1217
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RESULT 3

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US-09-286-529-19
; Sequence 19, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
```

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; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 1859
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-19
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Query Match      65.6%; Score 533.4; DB 4; Length 1859;
Best Local Similarity 98.9%; Pred. No. 1.9e-98;
Matches 537; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 1 GTGGCAGAAACACCACCTACCTCCCTGGGCGGAGCAGAGACAGGAGGAGGCTGTGTGC 60
Db 165 GTGGCAGAAACACCACCTACCTCCCTGGGCGGAGCAGAGAGAGAGGAGGAGGCTGTGTGC 224
QY 61 GCCCAGTGCCTCCCGGAGCAGCTTTGTGAGGAGGCGGCGCCGAGACAGCCCGACGAG 120
Db 225 GCCCAGTGCCTCCCGGAGCAGCTTTGTGAGGAGGCGGCGCCGAGACAGCCCGACGAG 284
QY 121 TGTGGCCCTGTGTCCACCGGCGCCTACGACGATTTCTGGAATCTGAGAGCTTGC 180
Db 285 TGTGGCCCTGTGTCCACCGGCGCCTACGACGATTTCTGGAATCTGAGAGCTTGC 344
QY 181 TACTGCAACGCTCTGTGGGGGAGCGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Db 345 TACTGCAACGCTCTGTGGGGGAGCGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 404
QY 241 AACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 405 AACCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
QY 301 GCATGCTGTCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db 465 GCATGCTGTCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 524
QY 361 TGCCAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 525 TGCCAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 584
QY 421 CCCGACCGCACTGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 585 CCCGACCGCACTGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 644
QY 481 GACACCTGTGTGACGACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 645 GACACCTGTGTGACGACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 704
QY 541 GAG 543
Db 705 GAG 707
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RESULT 4
US-09-286-529-7
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; Sequence 7, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-286-529-7
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Query Match      56.5%; Score 459; DB 4; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.2e-83;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 166 CTGAGAGCGTGTGCGGCTTCTGCAAGCTCTCTGTGGGGAGGCTGAGAGAGGAGGAGGAGG 225
Db 1 CTGAGAGCGTGTGCGGCTTCTGCAAGCTCTCTGTGGGGAGGCTGAGAGAGGAGGAGGAGGAGG 60
QY 226 TGCCAGCGCAACCCCAACCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 285
Db 61 TGCCAGCGCAACCCCAACCGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 286 TTCTGCTTGGAGCAGCGATCGTGTCCACTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCG 345
Db 121 TTCTGCTTGGAGCAGCGATCGTGTCCACTGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 346 AGCCGAAACACGAGTGTCCAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 405
Db 181 AGCCGAAACACGAGTGTCCAGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 406 TCGAGAGTGTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 465
Db 241 TCGAGAGTGTCCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 300
QY 466 GAGCTCTTCTCCCATGACACCTGTGTGACGAGCTGACGCTGCTGCTGCTGCTGCTGCTGCT 525
Db 301 GAGCTCTTCTCCCATGACACCTGTGTGACGAGCTGACGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 526 GTACAGAGCTGAGAGGTGTGAGCGTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 585
Db 361 GTACAGAGCTGAGAGGTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 586 TCCATCAAGAGGCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 624
Db 421 TCCATCAAGAGGCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 459
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RESULT 5
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US-08-997-918-47
; Sequence 47, Application US/08997918
; Patent No. 6077689
; GENERAL INFORMATION:
; APPLICANT: Snaively, Marshall D.
; TITLE OF INVENTION: ENHANCED SOLUBILITY OF RECOMBINANT PROTEINS
; FILE REFERENCE: A-496
; CURRENT APPLICATION NUMBER: US/08/997,918
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-08-997-918-47
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Query Match      15.9%; Score 129.6; DB 3; Length 525;
Best Local Similarity 53.6%; Pred. No. 7.2e-18;
Matches 270; Conservative 0; Mismatches 234; Indels 0; Gaps 0;
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QY 11 CACCCACCTACCTCCGCGGAGGAGCAGAGACAGGAGGAGCGGCTGTGTGGCCAGTGC 70
Db 14 CACCTAAATATCTTCATTATGATGAGAAACTGATCACAGCTGTGTGACAAATGTC 73
QY 71 CCCGAGCAGCTTTGTGTGACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 130
Db 74 CTCGGGTACTACTACTGAAACAGCAGCTGACCGCTTAATGAAAAACGTTTGGCTCTT 133
QY 131 GTCCAGCGGCGCACTACAGCAGAGTGTGAACTAAGTGAAGCGCTGCGCTACTGCAAG 190
Db 134 GTCCGAGCACTACTACACGAGCTCTGGCAGACCTCGAGAAATGCTGTACTGTCTAC 193
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QY 191 TCCTCTCGGGGAGCGTGAGGAGGACGCGGCTTGCCAGCCACCCACAAACCGTGCCT 250  
DB 194 CGGTTTTCAGGAGCGTGAGTACGTTAAACAGGAATGCAACCGTACGCAACCGTGTAT 253  
QY 251 GCCGCTGCCGACACCGGCTTCTCGCGACGCTGTTCTCTGTTGGAGCAGCATCGTGTG 310  
DB 254 GCGAATGCAAGAGGTGCTTACTCGAGATCGAATTTCTGCTGAACACCGTTCTCTGTC 313  
QY 311 CACCTGTGCGCGCGTGATTTGCCCGGACACCCCGAGCCAGAACACGAGTGCACCGCT 370  
DB 314 CGCCTGTTTCGCTGTGTACAGCTGTTACCGGTAACCGGTAACCGTGTGCAAAACGTT 373  
QY 371 GCCCGGACGACCTTCTAGCAGAGCTCCAGCTCAGAGCAGTGCACGCGCCACCGCA 430  
DB 374 GCCCGGACGCTTTCTTCTCAACGAAACCTCGAGCAAGCTCCGTTGCCGTAACACCA 433  
QY 431 ACTGCAGGCGCTGGGCTGGCCCTCAATGTGCCAGGCTTCTCTCCCATGACACCCCTGT 490  
DB 434 ACTGCTCCGTTTCGCTCTCTCTTTACCCAGAAAGTAACGCTACCCAGCAACATCT 493  
QY 491 GCACCAAGTGCACCTGCTTCCCC 514  
DB 494 GCTCCGTAACCTCCGAGTCGACCC 517

## RESULT 6

US-08-974-022-1  
; Sequence 1, Application US/08974022  
; Patent No. 6015938  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,022  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2432 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 124..1326  
; US-08-974-022-1

Query Match 13.8%; Score 112; DB 3; Length 2432;  
Best Local Similarity 52.3%; Pred. No. 2.8e-14;

Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;  
QY 31 GACGAGACAGGAGCGGCTGTTGCGCCAGTGCCTCCCGGAGCCTTTGTGAG 90  
DB 217 GACCCAGAAACCGGACGTCAGCTCTTGTGTGACAAATGTGCTCTGCGACCTACCTAAAA 276  
QY 91 CGGCGCTGCGCGGAGACAGCCCGGAGCGTGTGGCCGCTGTCCACCGCGCCACTACAG 150  
DB 277 CAGCACTGCACAGTACAGGAGGAAGACACTGTGTGCTCTTGCCTGACTACTCTTATACA 336  
QY 151 CAGTTCTGAACTACCTGGAGCGCTGCGCTACTGCAACGTCCTCTGCGGGAGCGGTGAG 210  
DB 337 GACAGCTGGCACACAGTGTGAAATGCGTGTACTGCGAGCCCGGTGTGCAAGGAACCTGAG 396  
QY 211 GAGGAGGACGGCTTGCACCGCACCCACACCGTGTGCGCTGCGCGTGCACCGCGCTTC 270  
DB 397 ACCGTGAAACAGGAGTGCACCCGACCCCAACCCAGTGTGCGAATGTGAGGAAGGCGC 456  
QY 271 TTCGCGCACGCTGTTTCTGCTTGGAGCAGCATCGTGTCCACTGTGCGCGCGTGATT 330  
DB 457 TACCTGGAGCTGCAATCTGCTTGAAGCACCGGAGCTGTCCCGAGCTTGGGTGTGCTG 516  
QY 331 GCCCGGCGACCCCGGAGCAGAACGAGTGCAGCCGTGCGCCCGGAGCAGCCTTCTCA 390  
DB 517 CAGGCTGGGACCCCGGAGCAGAACGAGTGTGCAAAAGATGTCCGGATGGGTCTTCTCA 576  
QY 391 GCCAGAGCTCCAGCTCAGAGCAGTCCAGCCCGGAGCCCGGAGTGCAGCGCGCTGGGCTG 450  
DB 577 GGTGAGACGTCATCGAAAGCACCCCTGTAGGAAACACACCAACTGCAGCTCACTTGGCTC 636  
QY 451 GCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGACACCAAGTCA 502  
DB 637 CTGCTAATTCAGAAAGGAATGCAACATGACATGTATGTTCGGAAACA 688

## RESULT 7

US-08-795-445A-1  
; Sequence 1, Application US/08795445A  
; Patent No. 628485  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Behavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,445A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2432 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single



TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 124..1326  
US-08-795-445A-1

Query Match 13.8%; Score 112; DB 4; Length 2432;  
Best Local Similarity 52.3%; Pred. No. 2.8e-14;  
Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 31 GACGAGAGACAGGGGAGCGGCTGTGTGCGCCAGTGCCTCCAGGACCTTTGTGACG 90  
DB 217 GACCCAGAAACCGAGCTGAGCTTGTGTGACAAATGTGTCTCTGACCTACTATAAA 276  
QY 91 CGGCGTGGCCCGCCAGACAGCCCAAGCTGTGTGCTCCAGCCGCGCACTAACAG 150  
DB 277 CAGCACTGCACTGACAGAGAGAAACAGTGTGTCTCTGCTGACTACTTATACA 336  
QY 151 CAGTTCTGAACTACTGAGCGCTGCGCTACTGCAAGCTCTCTGCGGAGAGCTGAG 210  
DB 337 GACAGCTGGACACAGATGATGATGTGTGTACTGACGCCCGGTGTGCAAGAACTGACG 396  
QY 211 GAGAGGACAGGGCTTGTGCAAGCCCAACCGTGTGCTGCGCTGCGGACCGGCTTC 270  
DB 397 ACCTGAAACAGAGAGTGAACCGGACCCAGACCGAGTGTGCAATGTGAGAAAGGCGC 456  
QY 271 TTGCGGACGCTGT 330  
DB 457 TACCTGAGCTGCAATTTCTGTGTGAAAGACCGAGCTGTCTCCAGGCTTGTGTGTGT 516  
QY 331 GCCCGGGGACCCCGACCGCAAGACAGCAAGTGCAGCGCTGCGCCCGGACGACCTTCTCA 390  
DB 517 CAGGCTGGAGCCCGAGAGCAACGTTTGTCAAAAGATGTCCGATGGTTTCTTCA 576  
QY 391 GCCAGAGCTCCAGCTCAGAGCAGTGCAGCCGCACTGACAGCGCTGCGGCTG 450  
DB 577 GGTGAGACGTGATGAAAGACCCCTGTAGGAAACACACAACTGACACTGTGGGCTC 636  
QY 451 GCCCTCATGTGCGAGGCTTCTCTCCATGACACCTGTGACACAGCTGCA 502  
DB 637 CTGCTAATTCAGAAAGAAATGCAACATGACATGTATGTTCGGAAACA 688

RESULT 8  
US-08-795-447A-1  
Sequence 1, Application US/08795447A  
Patent No. 6284728

## GENERAL INFORMATION:

APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: One Amgen Center Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91362-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795.447A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-37802  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2432 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 124..1326  
US-08-795-447A-1

Query Match 13.8%; Score 112; DB 4; Length 2432;  
Best Local Similarity 52.3%; Pred. No. 2.8e-14;  
Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 31 GACGAGAGACAGGGGAGCGGCTGTGTGCGCCAGTGCCTCCAGGACCTTTGTGACG 90  
DB 217 GACCCAGAAACCGAGCTGAGCTTGTGTGACAAATGTGTCTCTGACCTACTATAAA 276  
QY 91 CGGCGTGGCCCGCCAGACAGCCCAAGCTGTGTGCTCCAGCCGCGCACTAACAG 150  
DB 277 CAGCACTGCACTGACAGAGAGAAACAGTGTGTCTCTGCTGACTACTTATACA 336  
QY 151 CAGTTCTGAACTACTGAGCGCTGCGCTACTGCAAGCTCTCTGCGGAGAGCTGAG 210  
DB 337 GACAGCTGGACACAGATGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 396  
QY 211 GAGAGGACAGGGCTTGTGCAAGCCCAACCGTGTGCTGCGCTGCGGACCGGCTTC 270  
DB 397 ACCTGAAACAGAGAGTGAACCGGACCCAGACCGAGTGTGCAATGTGAGAAAGGCGC 456  
QY 271 TTGCGGACGCTGT 330  
DB 457 TACCTGAGCTGCAATTTCTGTGTGAAAGACCGAGCTGTCTCCAGGCTTGTGTGTGT 516  
QY 331 GCCCGGGGACCCCGACCGCAAGACAGCAAGTGCAGCGCTGCGCCCGGACGACCTTCTCA 390  
DB 517 CAGGCTGGAGCCCGAGAGCAACGTTTGTCAAAAGATGTCCGATGGTTTCTTCA 576  
QY 391 GCCAGAGCTCCAGCTCAGAGCAGTGCAGCCGCACTGACAGCGCTGCGGCTG 450  
DB 577 GGTGAGACGTGATGAAAGACCCCTGTAGGAAACACACAACTGACACTGTGGGCTC 636  
QY 451 GCCCTCATGTGCGAGGCTTCTCTCCATGACACCTGTGACACAGCTGCA 502  
DB 637 CTGCTAATTCAGAAAGAAATGCAACATGACATGTATGTTCGGAAACA 688

RESULT 9  
US-08-974-186-1  
Sequence 1, Application US/08974186  
Patent No. 6284740

## GENERAL INFORMATION:

APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Denavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30



APPLICANT: Boyle, William  
APPLICANT: Lacey, David  
APPLICANT: Calzone, Frank  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
FILE REFERENCE: A-378CIP  
CURRENT APPLICATION NUMBER: US/08/706,945D  
CURRENT FILING DATE: 1996-09-03  
PRIOR APPLICATION NUMBER: 08/577,788  
PRIOR FILING DATE: 1995-12-22  
NUMBER OF SEQ ID NOS: 145  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 123  
LENGTH: 2432  
TYPE: DNA  
ORGANISM: Rattus rattus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (124)..(1326)  
OTHER INFORMATION:  
US-08-706-945D-123

Query Match 13.8%; Score 112; DB 4; Length 2432;  
Best Local Similarity 52.3%; Pred. No. 2.8e-14;  
Matches 247; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 31 GACGACAGAGACAGGAGGAGCGCTGTGTGCGCCAGTGCCTCCAGGACCTTTGTGAG 90  
DB 217 GACCCAGAAACCGAGCTCCTTTGTGTACAAATGTGCTCTGACACTTACTTAAAA 276  
QY 91 CGGCGCTGCGCGGAGACAGCCCGACGCTGTGGCCCGTGTCCACCGCCACTACAG 150  
DB 277 CAGCAGCTGACAGTACAGAGAGAGACACTGTGTGCTTCCCTGAGCTACTTATACA 336  
QY 151 CAGTTCTGAACTACCTGAGCGCTGCGCTACTGCAACTCTCTCGGGAGCGTGA 210  
DB 337 GAGAGCTGGACACGAGTGTGATGTGTACTGACGCGCCCGTGTCAAGAACTGCAG 396  
QY 211 GAGAGGACAGGGGCTTCCAGCCAGCAGCAACCGTGTGCGCTGCGCGTCCGACCGGCTTC 270  
DB 397 ACCGTGAAAGAGAGTGAACCCGACCAACCGAGTGTGCAATTTGAGAAAGGCGC 456  
QY 271 TTGCGCAGCGCTGTGTTCTCTGTTGAGACGCACTGTGTCACCTGTGCGGCGTGA 330  
DB 457 TACCTGAGCTGCAATCTCTGTTGAAGACCGAGCTGTCCCGAGCTTGGGTGCTG 516  
QY 331 GCGCCGGGACCCCGACGAGACGCAAGTGCAGCGCGTGCCTCCGAGCACTTCTCA 390  
DB 517 CAGGCTGGAGCCCGACGAAACACCGTTTGCAGAAAGATGTCCGATGGGTTCTTCTCA 576  
QY 391 GCCAGAGCTCCAGCTGAGAGCACTGCGACCCGACCGCAACTGCAAGCGCTGGGCTG 450  
DB 577 GGTGAGCTGATCGAAAGACCTGTGAGAAACACACCACTGCACTTGGGCTC 636  
QY 451 GCCCTCAATGTGCGAGGCTTCTCTCCATGACACCTGTGACCACTGCA 502  
DB 637 CTGCTAATTCAGAAAGAAATGCAACATGACATATGTTCCGGAACA 688

RESULT 12  
US-08-974-022-3  
Sequence 3, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1324 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..1292  
US-08-974-022-3

Query Match 13.6%; Score 110.4; DB 3; Length 1324;  
Best Local Similarity 52.1%; Pred. No. 5.5e-14;  
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 31 GACGACAGAGACAGGAGGAGCGCTGTGTGCGCCAGTGCCTCCAGGACCTTTGTGAG 90  
DB 183 GACCCAGAAACGTATCATGCTCTGTGTGACAAATGTGCTCTGACACTTACTTAAAA 242  
QY 91 CGGCGCTGCGCGGAGACAGCCCGACGCTGTGGCCCGTGTCCACCGCCACTACAG 150  
DB 243 CAGCAGCTGACAGTGAAGAGAGAAACATGTGTCTTCCCTGAGCACTTATACG 302  
QY 151 CAGTTCTGAACTACCTGAGCGCTGCGCTACTGCAAGTCTCTGCGGGAGCGTGA 210  
DB 303 GAGAGCTGGACACAGTGTGATGTGTATTGACGCCAGTGTGCAAGAACTGTCAG 362  
QY 211 GAGAGGACAGGGCTTCCAGCCAGCAGCAACCGTGTGCTGCGCTGCGCAGCGCTTC 270  
DB 363 TCGTGAAGAGAGAGTGAACCGCACCCAGCAACCGAGTGTGATGTGAGAAAGGCGT 422  
QY 271 TTGCGCAGCGCTGTGTTCTCTGTTGAGACGCACTGTGTCACCTGTGCGGCGTGA 330  
DB 423 TACCTGAGATTCGAATTTCTGTTGAAGACCGGAGCTGTCCCGGAGCTCGGCGTGTG 482  
QY 331 GCGCCGGGACCCCGACGAGACGCAAGTGCAGCGCGTGCCTCCCGAGCACTTCTCA 390  
DB 483 CAGCTGGAACCCCGACGAAACACAGTTTGCAGAAAGATGTCAATGTGTTCTTCTCA 542  
QY 391 GCCAGAGCTCCAGCTGAGAGCACTGCGACCCGACCGCAACTGCAAGCGCTGGGCTG 450  
DB 543 GGTGAGCTTATCGAAAGACCTGTATTAACACACCAACTGCAAGCAATTTGGGCTC 602  
QY 451 GCCCTCAATGTGCGAGGCTTCTCTCCATGACACCTGTGACCACTGCA 502  
DB 603 CTGCTAATTCAGAAAGAAATGCAACATGACATGATGTTCCGGAACA 654

RESULT 13  
US-08-795-445A-3  
Sequence 3, Application US/08795445A  
Patent No. 6284485  
GENERAL INFORMATION:

APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,445A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1324 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..1292  
US-08-795-445A-3

Query Match 13.6%; Score 110.4; DB 4; Length 1324;  
Best Local Similarity 52.1%; Pred. No. 5.5e-14;  
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 31 GACGACAGACAGGGAGCGCTGGTGGCGCCAGTGCCTCCCGCCAGGACCTTTGTGCAG 90  
DB 183 GACCCAGAACTGGTTCATCAGCTCTGTGTGACAAATGTCTCTGGCACCTACCTAAAA 242

QY 91 CGGCGGTGCCCGGAGACAGCCCGACGACGTGTGGCGCGGTGTCCACCGCCACTACAG 150  
DB 243 CAGCACTGCACAGTGAAGGAGACATTTGTGTCTCCCTTGACCACTCTTATACG 302

QY 151 CAGTTCTGGAATCTAGGCGGTGGCGTCTACTGCAACGCTCTCGGGGAGCGGTGAG 210  
DB 363 TCCGTGAAGCAGAGTGAACCGCACCAACCGAGTGTGTGAGTGTGAGGAGGGCGT 422

QY 271 TTCGCGACGCTGGTTCTGTGGAGACGATCGTGTCCACTGTGTGCGCGGTGATT 330  
DB 423 TACCTGGAGATCGAATCTGCTTGAAGCAGCGAGCTGTCCCGGGGTCCGGGGTGGTG 482

QY 331 GCCCGGACCCCGCAGCAGACAGCGAGTGCAGCGCTGCCCGCCAGGACCTTCTCA 390  
DB 483 CAAGCTGGAACCCCGAGCGAACAACAGTTTGCAAAAAATTCAGATGGTTTCTTCA 542

QY 391 GCCAGCAGCTCCAGCTCAGAGCAGTGCAGCGCCCGCCAGCAACTGCAGCGCCCTGGCGTG 450  
DB 543 GGTGAGACTTCATCGAAGACCCCTGTATATAAACACACAGAACTGCAGCACATTTGGCCTC 602

QY 451 GCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACAGCTGCA 502

DB 603 CTGCTAATTCAGAAAGAAATGCAACACATGACAACTGTGTTCGGAACA 654

RESULT 14  
US-08-795-447A-3  
Sequence 3, Application US/08795447A  
Patent No. 6284728  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: One Amgen Center Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91362-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,447A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378D2  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1324 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..1292  
US-08-795-447A-3

Query Match 13.6%; Score 110.4; DB 4; Length 1324;  
Best Local Similarity 52.1%; Pred. No. 5.5e-14;  
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 31 GACGACAGACAGGGAGCGGTGGTGGCGCCAGTGCCTCCCGCCAGGACCTTTGTGCAG 90  
DB 183 GACCCAGAACTGGTTCATCAGCTCTGTGTGACAAATGTCTCTGGCACCTACCTAAAA 242

QY 91 CGGCGGTGCCCGGAGACAGCCCGACGACGTGTGGCGCGGTGTCCACCGCCACTACAG 150  
DB 243 CAGCACTGCACAGTGAAGGAGACATTTGTGTCTCCCTTGACCACTCTTATACG 302

QY 151 CAGTTCTGGAATCTAGGCGGTGGCGTCTACTGCAACGCTCTCGGGGAGCGGTGAG 210  
DB 303 GACAGTGGCACACCACTGATGATGTGTATTTGAGCCAGTGTGCAAGGAACCTGAG 362

QY 211 GAGAGGACAGCGGTGTGCGACGCAACCAACCGTGTGCGCTGCGCGTCCGACCGGCTTC 270  
DB 363 TCCGTGAAGCAGGAGTGAACCGCACCAACCGAGTGTGTGAGTGTGAGGAGGGCGT 422

QY 271 TTCGCGACGCTGGTTCTGTGGAGACGATCGTGTCCACTGTGTGCGCGGTGATT 330  
DB 423 TACCTGGAGATCGAATTTCTGCTTGAAGCAGCGAGCTGTCCCGGGGTCCGGGGTGGTG 482

QY 331 GCCCGGACCCCGCAGCAGACAGCGAGTGCAGCGCTGCCCGCCAGGACCTTCTCA 390  
DB 483 CAAGCTGGAACCCCGAGCGAACAACAGTTTGCAAAAAATTCAGATGGTTTCTTCA 542

QY 391 GCCAGCAGCTCCAGCTAGAGCAGTCCAGCCCAACCGCAATGACGAGCCCTGGGCTG 450  
DB 543 GGTGAGACTTCATGAAAGCAACCCCTGTATTAACACACAGAACTGACAGCACTTGGCCTG 602  
QY 451 GCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCTGTGACACCACTGCA 502  
DB 603 CTGCTAATTGAGAAAGAAATGCAACATGACACGCTGTGTCGGAAACA 654

## RESULT 15

US-08-974-186-3  
Sequence 3, Application US/08974186  
Patent No. 6284740  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Denavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,186  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1324 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..1292  
US-08-974-186-3

Query Match 13.6%; Score 110.4; DB 4; Length 1324;  
Best local similarity 52.1%; Pred. No. 5.5e-14;  
Matches 246; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 31 GACGACAGACAGAGGAGCGCTGTGTGCGCCAGTGCCTCCAGGACACCTTTGTGACG 90  
DB 183 GACCCAGAACTGTATCATCTCTGTGTGACAAATGTGCTCCTGACACTAATAA 242  
QY 91 CGGCGGCGCGCGCGAGACAGCCCAAGAGTGTGCGCGCTGTCCACCGCGCACTACAG 150  
DB 243 CAGACTGTGACAGTGAAGAGAAAGACATTTGTCTCTGCTGACCACTTTATACG 302  
QY 151 CAGTTTGAAGTCTGAGCGCTGCGGCTACTGCAAGCTCTGCGGGAGCGTGAAG 210  
DB 303 GACAGCTGGACACACATGATGATGTGTATTTGACCCAGTGTGCAAGAACTGACG 362  
QY 211 GAGAGGACAGGGGCTTGCACAGCCACCAACCGTGCCTGCGCGCTGCGACCGGCTTC 270

DB 363 TCCGTGAAGAGAGTGCACACCGCACCCACCAACGAGTGTGTGATGTGAGAAAGGCGT 422  
QY 271 TTGCGCAGCGCTGGTTTCTGCTTGAGACAGCAATCGTGTCCACTGGTGGCGGTGATT 330  
DB 423 TACCTGAGATCGAATTTCTGTGAGACACCGAGCTGTCCCGGGCTCGGGGTG 482  
QY 331 GCCCGGGCAACCCCAAGCAGAAACAGCAGTGCAGCGCTGCCCCCGGACACTTCTCA 390  
DB 483 CAAGCTGGAACCCCAAGAGCAACAGTTTGCAGAAATGTCAAGATGGGTTCTTCTCA 542  
QY 391 GCCAGCAGCTCCAGCTCAGAGCAGTGCAGCCCAACCGCACTGACAGGCTTGGGCTG 450  
DB 543 GGTGAGACTTCATGAAAGCAACCCCTGTATTAACACACGAACTGACACATTTGGCCTC 602  
QY 451 GCCCTCAATGTGCAGGCTCTTCTCCCATGACACCTGTGACACCACTGCA 502  
DB 603 CTGCTAATTGAGAAAGAAATGCAACATGACACGCTGTGTCGGAAACA 654

Search completed: January 6, 2003, 15:14:31  
Job time : 59 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 13:55:36 ; Search time 58 Seconds  
(without alignments)  
6062.518 Million cell updates/sec

Title: US-09-936-024-2

Perfect score: 813  
Sequence: 1 ggcgagcaaacaccacaccta.....agcgcttcctccctgtgcac 813

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:\*

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- 9: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq:\*
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- 11: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*
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- 13: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*
- 14: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	100.0	1077	10	US-09-935-727-1 Sequence 1, Appli
2	813	100.0	1114	10	US-09-896-096A-2 Sequence 2, Appli
3	813	100.0	1114	10	US-09-894-924-2 Sequence 2, Appli
4	813	100.0	1347	10	US-09-877-156-18 Sequence 18, Appli
5	809.4	99.6	1137	10	US-09-840-795-1 Sequence 7, Appli
6	533.4	65.6	1859	10	US-09-877-156-19 Sequence 12, Appli
7	515.4	63.4	903	10	US-09-935-727-32 Sequence 32, Appli
8	473.4	58.2	491	10	US-09-896-096A-3 Sequence 3, Appli
9	473.4	58.2	491	10	US-09-894-924-3 Sequence 3, Appli
10	459	56.5	459	10	US-09-877-156-7 Sequence 3, Appli
11	392.2	48.2	1550	10	US-09-935-727-33 Sequence 33, Appli
12	387.4	47.7	1667	10	US-09-935-727-3 Sequence 33, Appli
13	387	47.6	1796	10	US-09-935-727-28 Sequence 28, Appli
14	245.2	30.2	271	10	US-09-894-924-5 Sequence 5, Appli
15	245.2	30.2	271	10	US-09-894-924-5 Sequence 5, Appli
16	242.2	29.8	283	10	US-09-896-096A-10 Sequence 10, Appli
17	242.2	29.8	283	10	US-09-894-924-10 Sequence 10, Appli
18	220.8	27.2	499	10	US-09-935-727-17 Sequence 17, Appli
19	218.8	26.9	226	10	US-09-896-096A-9 Sequence 9, Appli

20	218.8	26.9	226	10	US-09-894-924-9	Sequence 9, Appli
21	200	24.6	201	10	US-09-896-096A-6	Sequence 6, Appli
22	200	24.6	201	10	US-09-894-924-6	Sequence 6, Appli
23	194.2	23.9	199	10	US-09-896-096A-8	Sequence 8, Appli
24	194.2	23.9	199	10	US-09-894-924-8	Sequence 8, Appli
25	183	22.5	233	9	US-09-292-758-141	Sequence 141, Appli
26	179	22.0	191	10	US-09-935-727-18	Sequence 18, Appli
27	152.2	18.7	277	10	US-09-896-096A-7	Sequence 7, Appli
28	152.2	18.7	277	10	US-09-894-924-7	Sequence 7, Appli
29	103.4	12.7	564	10	US-09-062-113-102	Sequence 102, Appli
30	103	12.7	594	10	US-09-062-113-97	Sequence 97, Appli
31	103	12.7	819	10	US-09-062-113-96	Sequence 96, Appli
32	103	12.7	966	10	US-09-062-113-101	Sequence 101, App
33	103	12.7	981	10	US-09-062-113-92	Sequence 92, Appli
34	103	12.7	984	10	US-09-062-113-93	Sequence 93, Appli
35	103	12.7	1056	10	US-09-062-113-95	Sequence 95, Appli
36	103	12.7	1089	10	US-09-062-113-100	Sequence 100, App
37	103	12.7	1182	10	US-09-062-113-94	Sequence 94, Appli
38	103	12.7	1200	12	US-10-105-934-3	Sequence 3, Appli
39	103	12.7	1303	12	US-10-105-934-3	Sequence 3, Appli
40	103	12.7	1206	10	US-09-062-113-6	Sequence 6, Appli
41	103	12.7	1206	10	US-09-062-113-83	Sequence 83, Appli
42	103	12.7	1206	10	US-09-062-113-84	Sequence 84, Appli
43	103	12.7	1206	10	US-09-062-113-85	Sequence 85, Appli
44	103	12.7	1206	10	US-09-062-113-86	Sequence 86, Appli
45	103	12.7	1206	10	US-09-062-113-87	Sequence 87, Appli

#### ALIGNMENTS

RESULT 1  
US-09-935-727-1  
Sequence 1, Application US/09935727  
Patent No. US20020150583A1  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
FILE REFERENCE: P4454P2  
CURRENT APPLICATION NUMBER: US/09/935,727  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 60/303,224  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: 60/252,131  
PRIOR FILING DATE: 2000-11-21  
PRIOR APPLICATION NUMBER: 60/227,598  
PRIOR FILING DATE: 2000-08-25  
PRIOR APPLICATION NUMBER: 09/518,931  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: 60/168,235  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 60/146,371  
PRIOR FILING DATE: 1999-08-02  
PRIOR APPLICATION NUMBER: 60/131,964  
PRIOR FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: 60/131,270  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/124,092  
PRIOR FILING DATE: 1999-03-12  
PRIOR APPLICATION NUMBER: 60/121,774  
PRIOR FILING DATE: 1999-03-04  
PRIOR APPLICATION NUMBER: 09/006,352  
PRIOR FILING DATE: 1998-01-13  
PRIOR APPLICATION NUMBER: 60/035,496  
PRIOR FILING DATE: 1997-01-14  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1077  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS

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; LOCATION: (25)...(924)
US-09-935-727-1

Query Match      100.0%; Score 813; DB 10; Length 1077;
Best Local Similarity 100.0%; Pred. No. 7.8e-162;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGGAGCGGCTGGTGTC 60
DB 112 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGGAGCGGCTGGTGTC 171

QY 61 GCCAGTGCCCGCCAGGACCTTTGTGACGCGCGGTGGCCGAGACAGCCACGACG 120
DB 172 GCCAGTGCCCGCCAGGACCTTTGTGACGCGCGGTGGCCGAGACAGCCACGACG 231

QY 121 TGTGGCCCGGTGTCCACCGCCCACTACACGAGTTCTGGAACCTCTGGAGCGCTGCCGC 180
DB 232 TGTGGCCCGGTGTCCACCGCCCACTACACGAGTTCTGGAACCTCTGGAGCGCTGCCGC 291

QY 181 TACTGCAACCTCTCTGCGGGAGCGTGTGAGGAGGACGCGGCTTGCCACGCCACCCAC 240
DB 292 TACTGCAACCTCTCTGCGGGAGCGTGTGAGGAGGACGCGGCTTGCCACGCCACCCAC 351

QY 241 AACGTCGCTGCCGCTGCCGACCGGCTTCTGCGCACGCTGTTCTGCTTGGAGCAC 300
DB 352 AACGTCGCTGCCGCTGCCGACCGGCTTCTGCGCACGCTGTTCTGCTTGGAGCAC 411

QY 301 GCATCGTGTCCACCTGTGCGCGGTGATTGGCCCGGGACACCCCGAGCAACAGCAG 360
DB 412 GCATCGTGTCCACCTGTGCGCGGTGATTGGCCCGGGACACCCCGAGCAACAGCAG 471

QY 361 TGCAGCGCTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAG 420
DB 472 TGCAGCGCTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAG 531

QY 421 CCCCACCGCAACTGCAAGCGCCCTGGGCGCTGCGCCCTCAATGTGCAGGCTCTCTCCCTCCAT 480
DB 532 CCCCACCGCAACTGCAAGCGCCCTGGGCGCTGCGCCCTCAATGTGCAGGCTCTCTCCCTCCAT 591

QY 481 GACACCTGTGCACCACTGCACTGGCTTCCCTCTCAGCACCAGGATACAGGAGCTGAG 540
DB 592 GACACCTGTGCACCACTGCACTGGCTTCCCTCTCAGCACCAGGATACAGGAGCTGAG 651

QY 541 GAGTGTAGCGCTGCCGTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGCTG 600
DB 652 GAGTGTAGCGCTGCCGTCATCGACTTTGTGGCTTTCAGGACATCTCCATCAAGAGCTG 711

QY 601 CAGCGGCTGTGCAGCGCCCTCGAGGCGCCCGAGGCGCTGGGGTCCGACACCAAGGCGGGC 660
DB 712 CAGCGGCTGTGCAGGCGCCCTCGAGGCGCCCGAGGCGCTGGGGTCCGACACCAAGGCGGGC 771

QY 661 CGCGCGGCTTTCAGCTGAAAGCTGCGTGGCGGCTCAGCGAGCTCTCTGGGGGCGCAGGAC 720
DB 772 CGCGCGGCTTTCAGCTGAAAGCTGCGTGGCGGCTCAGCGAGCTCTCTGGGGGCGCAGGAC 831

QY 721 GGGCGCTGTGTGTGCGGCTGTGTCAGGCGCTGCGGTGCGCAGGATGCCCGGCTGGAG 780
DB 832 GGGCGCTGTGTGTGCGGCTGTGTCAGGCGCTGCGGTGCGCAGGATGCCCGGCTGGAG 891

QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 813
DB 892 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 924
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RESULT 2

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US-09-896-096A-2
; Sequence 2, Application US/09896096A
; Patent No. US20020061559A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
```

```
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: FITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DcE3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 1090
; OTHER INFORMATION: Unknown base
US-09-896-096A-2

Query Match      100.0%; Score 813; DB 10; Length 1114;
Best Local Similarity 100.0%; Pred. No. 7.8e-162;
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGGAGCGGCTGGTGTC 60
DB 188 GTGGCAGAAACACCCACCTACCCCTGGCGGAGCGAGACAGAGGAGCGGCTGGTGTC 247

QY 61 GCCAGTGCCCGCCAGGACCTTTGTGACGCGCGCTGCGCGAGACAGCCACGACG 120
DB 248 GCCAGTGCCCGCCAGGACCTTTGTGACGCGCGCTGCGCGAGACAGCCACGACG 307

QY 121 TGTGGCCCGGTGTCCACCGCCCACTACACGCACTTCTGGAACCTACCTGGAGCGCTGCCGC 180
DB 308 TGTGGCCCGGTGTCCACCGCCCACTACACGCACTTCTGGAACCTACCTGGAGCGCTGCCGC 367

QY 181 TACTGCAACGCTCTCTGCGGGAGCGTGTGAGGAGGACGCGGCTTGCCACGCCACCCAC 240
DB 368 TACTGCAACGCTCTCTGCGGGAGCGTGTGAGGAGGACGCGGCTTGCCACGCCACCCAC 427

QY 241 AACCGTGCCTGCGCGCTGCGCACCGGCTTCTTCCGCGCAGCTGGTTCCTGCTTGGAGCAC 300
DB 428 AACCGTGCCTGCGCGCTGCGCACCGGCTTCTTCCGCGCAGCTGGTTCCTGCTTGGAGCAC 487

QY 301 GCATCGTGTCCACCTGGTGGCGCGGTGATTGCCCGGGGACACCCCGAGCAACAGCAG 360
DB 488 GCATCGTGTCCACCTGGTGGCGCGGTGATTGCCCGGGGACACCCCGAGCAACAGCAG 547

QY 361 TGCAGCGCTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAG 420
DB 548 TGCAGCGCTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCAG 607

QY 421 CCCCACCGCAACTGCAAGCGCCCTGGGCGCTTCAATGTGCAGGCTCTCTCCCTCCAT 480
DB 608 CCCCACCGCAACTGCAAGCGCCCTGGGCGCTTCAATGTGCAGGCTCTCTCCCTCCAT 667

QY 481 GACACCTGTGCACCACTGCACTGGCTTCCCCCTCAGCACCAGGATACAGAGCTGAG 540
DB 668 GACACCTGTGCACCACTGCACTGGCTTCCCCCTCAGCACCAGGATACAGAGCTGAG 727

QY 541 GAGTGTAGCGCTGCCGTCATCGACTTTGTGGCTTTCAGAGCACTCTCCATCAAGAGCTG 600
DB 728 GAGTGTAGCGCTGCCGTCATCGACTTTGTGGCTTTCAGAGCACTCTCCATCAAGAGCTG 787

QY 601 CAGCGGCTGTGTCAGGCGCTTCCAGGCGCCCGAGGCGCTGGGGTCCGACACCAAGGCGGGC 660
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Db 788 CAGCGCTCTGTCAGAGCCCTTCAGAGCCCGAGGAGGCTGGGGTCCGACACCAAGGGCGGGC 847  
Qy 661 CGCGCGCTTGTGACGCTGAAGCTGCTGCGGCTCAAGAGCTCTTGGGGCGCAGAGC 720  
Db 848 CGCGCGCTTGTGACGCTGAAGCTGCTGCGGCTCAAGAGCTCTTGGGGCGCAGAGC 907  
Qy 721 GGGGCGCTGCTGTCGAGCTGCTGTCAGAGCGCTGCGCTGGCCAGAGATGCCGGGCTGGAG 780  
Db 908 GGGGCGCTGCTGTCGAGCTGCTGTCAGAGCGCTGCGCTGGCCAGAGATGCCGGGCTGGAG 967  
Qy 781 CGAGAGCTCCGTGAGCGCTTCTCTCTGTGCAC 813  
Db 968 CGAGAGCTCCGTGAGCGCTTCTCTCTGTGCAC 1000

RESULT 3  
US-09-894-924-2  
; Sequence 2, Application US/09894924  
; Patent No. US20020065210A1  
; GENERAL INFORMATION:  
; APPLICANT: ASHKENAZI, AVI J  
; APPLICANT: BOTSHEIN, DAVID  
; APPLICANT: DODGE, KELLY H.  
; APPLICANT: GURNEY, AUSTIN L.  
; APPLICANT: KIM, KYUNG JIN  
; APPLICANT: LAWRENCE, DAVID A.  
; APPLICANT: PITTI, ROBERT  
; APPLICANT: ROY, MARGARET A  
; APPLICANT: TOMAS, DANIEL B  
; APPLICANT: WOOD, WILLIAM I.  
; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog  
; FILE REFERENCE: P1134R2 REVISED  
; CURRENT APPLICATION NUMBER: US/09/894,924  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/157,289  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: US 60/059,288  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: US 60/094,640  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 18  
; SEQ ID NO 2  
; LENGTH: 1114  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: 1090  
; OTHER INFORMATION: Unknown base  
US-09-894-924-2

Query Match 100.0%; Score 813; DB 10; Length 1114;  
Best Local Similarity 100.0%; Pred. No. 7,8e-162;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGCAGAAAACACCCTACCTCTGGCGGAGCCAGACAGAGGAGGCGGCTGTGTGC 60  
Db 188 GTGGCAGAAAACACCCTACCTCTGGCGGAGCCAGACAGAGGAGGCGGCTGTGTGC 247  
Qy 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGCGCCGACAGACAGCCAGACG 120  
Db 248 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGCGCCGACAGACAGCCAGACG 307  
Qy 121 TGTGGCCCGTGTCCACCGCGCCTACACGAGTTCTGGAATCTCTGAGCGCTGCCGC 180  
Db 308 TGTGGCCCGTGTCCACCGCGCCTACACGAGTTCTGGAATCTCTGAGCGCTGCCGC 367  
Qy 181 TACTGCAACGCTCTCTGTGGGAGCGTAGAGAGGAGCGAGGCTTGGCAAGCCAC 240  
Db 368 TACTGCAACGCTCTCTGTGGGAGCGTAGAGAGGAGCGAGGCTTGGCAAGCCAC 427  
Qy 241 AACCGTCTGCTGCTGCGCAGCGGCTTCTTGGCGACGCTGTGTTCTGTGAGAGC 300

Db 428 AACCGTCTGCTGCTGCGCAGCGGCTTCTTGGCGACGCTGTGTTCTGTGAGAC 487  
Qy 301 GCATCGTGTCCACCTGATGCGGCGGTGATGCCCGGACCCCGACAGCAACAGCAG 360  
Db 488 GCATCGTGTCCACCTGATGCGGCGGTGATGCCCGGACCCCGACAGCAACAGCAG 547  
Qy 361 TGCACGCGTGGCCCCCAGGACCTTCTGACGACAGCTTCAGAGCAAGTGCAG 420  
Db 548 TGCACGCGTGGCCCCCAGGACCTTCTGACGACAGCTTCAGAGCAAGTGCAG 607  
Qy 421 CCCCACCGCAATGCAAGGCGCTGCGGCTGAGCCCTCAATGTGCAAGCTTCTCCAT 480  
Db 608 CCCCACCGCAATGCAAGGCGCTGCGGCTGAGCCCTCAATGTGCAAGCTTCTCCAT 667  
Qy 481 GACACCTGTGACAGCTGACATGAGCTTCCCTCAGACAGAGGATCCAGAGAGCTG 540  
Db 668 GACACCTGTGACAGCTGACATGAGCTTCCCTCAGACAGAGGATCCAGAGAGCTG 727  
Qy 541 GAGTGTAGGCTGCGGCTGATGACCTTGTGAGCTTTCAGAGACATTCATCAAGAGCTG 600  
Db 728 GAGTGTAGGCTGCGGCTGATGACCTTGTGAGCTTTCAGAGACATTCATCAAGAGCTG 787  
Qy 601 CAGCGGCTGCTGACAGGCGCTTCAGAGCCCGGAGGAGCTGGGCTCCAGACCAAGGCGGCG 660  
Db 788 CAGCGGCTGCTGACAGGCGCTTCAGAGCCCGGAGGAGCTGGGCTCCAGACCAAGGCGGCG 847  
Qy 661 CGCGCGCTTGTGACGCTGAAGCTGCGGCTGCGGCTCAAGAGCTCTTGGGGCGCAGAGC 720  
Db 848 CGCGCGCTTGTGACGCTGAAGCTGCGGCTGCGGCTCAAGAGCTCTTGGGGCGCAGAGC 907  
Qy 721 GGGGCGCTGCTGTCGCTGCTGTCAGAGCGCTGCGCTGCGCAGAGATGCCGGGCTGGAG 780  
Db 908 GGGGCGCTGCTGTCGCTGCTGTCAGAGCGCTGCGCTGCGCAGAGATGCCGGGCTGGAG 967  
Qy 781 CGAGAGCTCCGTGAGCGCTTCTCTGTGCAC 813  
Db 968 CGAGAGCTCCGTGAGCGCTTCTCTGTGCAC 1000

RESULT 4  
US-09-877-156-18  
; Sequence 18, Application US/09877156  
; Patent No. US20020055625A1  
; GENERAL INFORMATION:  
; APPLICANT: Catherine Tribouley  
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
; FILE REFERENCE: 1408.003/200130.439C1  
; CURRENT APPLICATION NUMBER: US/09/877,156  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 09/286,529  
; PRIOR FILING DATE: 1998-04-05  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 1347  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-877-156-18

Query Match 100.0%; Score 813; DB 10; Length 1347;  
Best Local Similarity 100.0%; Pred. No. 8e-162;  
Matches 813; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGCAGAAAACACCCTACCTCTGGCGGAGCCAGACAGAGGAGGCGGCTGTGTGC 60  
Db 405 GTGGCAGAAAACACCCTACCTCTGGCGGAGCCAGACAGAGGAGGCGGCTGTGTGC 464  
Qy 61 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGCGCCGACAGACAGCCAGACG 120  
Db 465 GCCCAGTGGCCCCCAGGACCTTTGTGACGCGCGCTGCGCCGACAGACAGCCAGACG 524  
Qy 121 TGTGGCCCGTGTCCACCGCGCCTACACGAGTTCTGGAATCTCTGAGCGCTGCCGC 180

D	b	525	TGTGGCCGGTGTCCACGGCGCCACTACACGAGTCTTGGAATCTACTGGAGCGCTGCCGC	584
Q	y	181	TACTGCAACCTCTCTTCGCGGGAGCGTGAGGAGGAGCA	240
D	b	585	TACTGCAACGCTCTCTCGCGGAGCGTGAGGAGGAGGAC	644
Q	y	241	AACGGTGCCTGCGCTGCGCGACCGGCTTCTTCGCGCAGCTGGTTCCTGCTTGGAGCAC	300
D	b	645	AACCGTGCCTTGGCGCTGCGCGACCGGCTTCTTCGCGCAGCTGGTTCCTGCTTGGAGCAC	704
Q	y	301	GCATCGTGTCCACCTGGTGC	360
D	b	705	GCATCGTGTCCACCTGGTGC	764
Q	y	361	TGCGAGCGGTGCCCGCCAGGACCTTCTCAGCCAGGAGGTC	420
D	b	765	TGCGAGCGGTGCCCGCCAGGACCTTCTCAGCCAGGAGGTC	824
Q	y	421	CCCCACCGCAACTGCAGCGGCCCTGGGCCCTCAATGTGCCAGGCTCTTCTCTCCCAT	480
D	b	825	CCCCACCGCAACTGCAGCGGCCCTGGGCCCTCAATGTGCCAGGCTCTTCTCTCCCAT	884
Q	y	481	GACACCTGTGCACACAGCTGCATGTGCTTCCCCCTCAGCAC	540
D	b	885	GACACCTGTGCACACAGCTGCATGTGCTTCCCCCTCAGCAC	944
Q	y	541	GAGTGTGAGCGTGCGCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGCGTG	600
D	b	945	GAGTGTGAGCGTGCGCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGCGTG	1004
Q	y	601	CAGCGGCTGTGACAGGCCCTTCAGAGGCCCGGAGGGCTGGGGTCCGACAC	660
D	b	1005	CAGCGGCTGTGACAGGCCCTTCAGAGGCCCGGAGGGCTGGGGTCCGACAC	1064
Q	y	661	CGCGCGGCTTGCAGCTGAAGCTGCGTCCGGCGGCTCA	720
D	b	1065	CGCGCGGCTTGCAGCTGAAGCTGCGTCCGGCGGCTCA	1124
Q	y	721	GGGGCGCTGTGTTGGCGCTGTGACAGGCGCTGCGCGTGGCCAGGATCCCGCGGCTGGAG	780
D	b	1125	GGGGCGCTGTGTTGGCGCTGTGACAGGCGCTGCGCGTGGCCAGGATCCCGCGGCTGGAG	1184
Q	y	781	CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC	813
D	b	1185	CGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC	1217

## RESULT 5

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US-09-840-795-1
; Sequence 1, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Erin E.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Bates, Elizabeth Esther Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Genes; Related Reagents
; FILE REFERENCE: SP0818K
; CURRENT APPLICATION NUMBER: US/09/840,795
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: primate
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)..(998)
; NAME/KEY: misc feature

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; LOCATION: (367)
; OTHER INFORMATION: W; may be A or T
; NAME/KEY: mat_peptide
; LOCATION: (132) .. (998)
US-09-840-795-1

Query March          99.6%; Score 809.4; DB 10; Length 1137;
Best Local Similarity 99.6%; Pred. No. 4.4e-161;
Matches 810; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGGCAGAAAACACCCACCTACCTCTGGCGGACGCAGAGACAGGAGCGCGTGGTGTGC 60
DB 186 GTGGCAGAAAACACCCACCTACCTCTGGCGGAGCGCAGAGACAGGAGCGCGTGGTGTGC 245
-QY 61 GCCCAGTCCCCCCCAGGCACCTTTGTGACGGCGCGTGCCTCCGAGACAGCCCCACGACG 120
DB 246 GCCCAGTCCCCCCCAGGCACCTTTGTGACGGCGCGTGCCTCCGAGACAGCCCCATGACG 305
QY 121 TGTGCCCGGTGTACACCGGCGCACTACACGCAGTTCTGGAACTACTTGGAGCGGTGCCGC 180
DB 306 TGTGCCCGGTGTACACCGGCGCACTACACGCAGTTCTGGAACTACTTGGAGCGGTGCCGC 365
QY 181 TACTTCAACGTCTCTCTGCGGGGAGCGGTGAGGAGGAGGACCGGGTGTGCACGCGCACCCAC 240
DB 366 TWTGCTACGTCTCTCTGCGGGGAGCGGTGAGGAGGAGGACCGGGTGTGCACGCGCACCCAC 425
QY 241 AACCGTGCCTCCGCTGCCGACCGCGTTCTTCGCGCACGCTGTGTTCTGTGGAGCAC 300
DB 426 AACCGTGCCTCCGCTGCCGACCGCGTTCTTCGCGCACGCTGTGTTCTGTGGAGCAC 485
QY 301 GCATCGTGTCCACTGTGTCCGGGTGATTTGCCCGGGCACCCCCAGCGCAAAACGCGAG 360
DB 486 GCATCGTGTCCACTGTGTCCGGGTGATTTGCCCGGGCACCCCCAGCGCAAAACGCGAG 545
QY 361 TGCCAGCCGTGCCCCCAGGACCTTCTCAGCAGCAGCTCCAGCTCAGAGCAGTGCCAG 420
DB 546 TGCCAGCCGTGCCCCCAGGACCTTCTCAGCAGCAGCTCCAGCTCAGAGCAGTGCCAG 605
QY 421 CCCCACCGCAATGCAACGCGCCTGGCGTGGCCTCAATGTGCCAGGCTCTTCCTCCCAT 480
DB 606 CCCCACCGCAATGCAACGCGCCTGGCGTGGCCTCAATGTGCCAGGCTCTTCCTCCCAT 665
QY 481 GACACCTGTGCACCGCTGCACTGGCTTCCCTCTCAGCACACAGGTTACGAGAGCTGAG 540
DB 666 GACACCTGTGCACCGCTGCACTGGCTTCCCTCTCAGCACACAGGTTACGAGAGCTGAG 725
QY 541 GAGTGTAGCGTCCGCTCATCGACTTTGTGGCTTTCAGAGCACATCTCCATCAAGAGGCTG 600
DB 726 GAGTGTAGCGTCCGCTCATCGACTTTGTGGCTTTCAGAGCACATCTCCATCAAGAGGCTG 785
QY 601 CAGCGGCTGTCTCAGGCGCTTCAGGCGCCCGAGGCGTGGGTTCGCACACCAAGGCGCGGC 660
DB 786 CAGCGGCTGTCTCAGGCGCTTCAGGCGCCCGAGGCGTGGGTTCGCACACCAAGGCGCGGC 845
QY 661 CGCGGGCGCTTTCAGCTGAAGCTGGTCCGCGCTCAGGAGCTCCTGGGGCGCGAGAC 720
DB 846 CGCGGGCGCTTTCAGCTGAAGCTGGTCCGCGCTCAGGAGCTCCTGGGGCGCGAGAC 905
QY 721 GGGGCGCTGTCTGGTGCAGCGCTGTGAGCGCTTGGCGCTGGCGAGGATGCCCGGGCTGGAG 780
DB 906 GGGGCGCTGTCTGGTGCAGCGCTGTGAGCGCTTGGCGTGGCGAGGATGCCCGGGCTGGAG 965
QY 781 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAAC 813
DB 966 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAAC 998

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## RESULT 6

US-09-877-156-19  
; Sequence 19, Application US/09877156  
; Patent No. US20020055625A1  
; GENERAL INFORMATION:  
; APPLICANT: Catherine Tribouley

;; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
;; FILE REFERENCE: 1408.003/200130.439C1  
;; CURRENT APPLICATION NUMBER: US/09/877.156  
;; PRIOR FILING DATE: 2001-06-08  
;; PRIOR APPLICATION NUMBER: US 09/286,529  
;; PRIOR FILING DATE: 1998-04-05  
;; NUMBER OF SEQ ID NOS: 25  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO: 19  
;; LENGTH: 1859  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-09-877-156-19

Query Match 65.6%; Score 533.4; DB 10; Length 1859;  
Best Local Similarity 98.9%; Pred. No. 2,6e-103;  
Matches 537; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GTGGGAGAAACACCCCTTACCCCTGGCGGAGACGACAGACAGGAGCGGCTGTGTC 60  
DB 165 GTGGGAGAAACACCCCTTACCCCTGGCGGAGACGACAGACAGGAGCGGCTGTGTC 224  
QY 61 GCGCAGTGGCCCGCCAGGACCTTTGTGAGGCGGCTGCCCGGACAGACGCCCAAGAC 120  
DB 225 GCGCAGTGGCCCGCCAGGACCTTTGTGAGGCGGCTGCCCGGACAGACGCCCAAGAC 284  
QY 121 TGTGGCCCGTGTCCAGCGCGGACCTACACGAGTTCTGGAATCTAGGAGCGTGCAGC 180  
DB 285 TGTGGCCCGTGTCCAGCGCGGACCTACACGAGTTCTGGAATCTAGGAGCGTGCAGC 344  
QY 181 TACTGCAACGTCCTCTGTGGGAGCGGTGAGAGAGAGGACGCGGCTTGCCAGCCAC 240  
DB 345 TACTGCAACGTCCTCTGTGGGAGCGGTGAGAGAGAGGACGCGGCTTGCCAGCCAC 404  
QY 241 AACGTCGCTGCGGCTGCGGACCGGCTTCTTCCGCGACGCTGTGTTCTGTGAGCAC 300  
DB 405 AACGTCGCTGCGGCTGCGGACCGGCTTCTTCCGCGACGCTGTGTTCTGTGAGCAC 464  
QY 301 GCATCGTGTCCACCTGTGGGCGGCGGTATTTGCCCGGACCGCCAGCCAGAACGCGAG 360  
DB 465 GCATCGTGTCCACCTGTGGGCGGCGGTATTTGCCCGGACCGCCAGCCAGAACGCGAG 524  
QY 361 TGCCAGCGTGTGCGGCGGACGCTTCTCAAGCAGACGCTTCAAGCAGTGCAG 420  
DB 525 TGCCAGCGTGTGCGGCGGACGCTTCTCAAGCAGACGCTTCAAGCAGTGCAG 584  
QY 421 CCCACCGCACTGCAAGCGGCTTGGGCTGAGCTTCAATGTGCCAGGCTTCTTCCCAT 480  
DB 585 CCCACCGCACTGCAAGCGGCTTGGGCTGAGCTTCAATGTGCCAGGCTTCTTCCCAT 644  
QY 481 GACACCGTGTGCAAGCTGTGAGCTTCCCTCAAGCAGACGAGGTACCGAGAGCTGAG 540  
DB 645 GACACCGTGTGCAAGCTGTGAGCTTCCCTCAAGCAGACGAGGTACCGAGAGCTGAG 704  
QY 541 GAG 543  
DB 705 GAG 707

RESULT 7  
US-09-935-727-32  
; Sequence 32, Application US/09935727  
; Patent No. US20020150583A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta  
; FILE REFERENCE: PF454P2  
; CURRENT APPLICATION NUMBER: US/09/935.727  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/303,224  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: 60/252,131  
; PRIOR FILING DATE: 2000-11-21

;; PRIOR APPLICATION NUMBER: 60/227,598  
;; PRIOR FILING DATE: 2000-08-25  
;; PRIOR APPLICATION NUMBER: 09/518,931  
;; PRIOR FILING DATE: 2000-03-03  
;; PRIOR APPLICATION NUMBER: 60/168,235  
;; PRIOR FILING DATE: 1999-12-01  
;; PRIOR APPLICATION NUMBER: 60/146,371  
;; PRIOR FILING DATE: 1999-08-02  
;; PRIOR APPLICATION NUMBER: 60/131,964  
;; PRIOR FILING DATE: 1999-04-30  
;; PRIOR APPLICATION NUMBER: 60/131,270  
;; PRIOR FILING DATE: 1999-04-27  
;; PRIOR APPLICATION NUMBER: 60/124,092  
;; PRIOR FILING DATE: 1999-03-12  
;; PRIOR APPLICATION NUMBER: 60/121,774  
;; PRIOR FILING DATE: 1999-03-04  
;; PRIOR APPLICATION NUMBER: 09/006,352  
;; PRIOR FILING DATE: 1998-01-13  
;; PRIOR APPLICATION NUMBER: 60/035,496  
;; PRIOR FILING DATE: 1997-01-14  
;; NUMBER OF SEQ ID NOS: 42  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO: 32  
;; LENGTH: 903  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Mammalian synthetic TNFR-6 alpha  
US-09-935-727-32

Query Match 63.4%; Score 515.4; DB 10; Length 903;  
Best Local Similarity 77.1%; Pred. No. 1.4e-99;  
Matches 627; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 1 GTGGGAGAAACACCCCTTACCCCTGGCGGAGACGACAGACAGGAGCGGCTGTGTC 60  
DB 88 GTGGGAGAAACACCCCTTACCCCTGGCGGAGACGACAGACAGGAGCGGCTGTGTC 147  
QY 61 GCGCAGTGGCCCGCCAGGACCTTTGTGAGGCGGCTGCCCGGACAGACGCCCAAGAC 120  
DB 148 GCGCAGTGGCCCGCCAGGACCTTTGTGAGGCGGCTGCCCGGACAGACGCCCAAGAC 207  
QY 121 TGTGGCCCGTGTCCAGCGCGGACCTTGTGAGGCGGCTGCCCGGACAGACGCCCAAGAC 180  
DB 208 TGTGGCCCGTGTCCAGCGCGGACCTTGTGAGGCGGCTGCCCGGACAGACGCCCAAGAC 267  
QY 181 TACTGCAACGTCCTCTGTGGGAGCGGTGAGAGAGGACGCGGCTTGCCAGCCAC 240  
DB 268 TACTGCAACGTCCTCTGTGGGAGCGGTGAGAGAGGACGCGGCTTGCCAGCCAC 327  
QY 241 AACGTCGCTGCGGCTGCGGACCGGCTTCTTCCGCGACGCTGTGTTCTGTGAGCAC 300  
DB 328 AACGTCGCTGCGGCTGCGGACCGGCTTCTTCCGCGACGCTGTGTTCTGTGAGCAC 387  
QY 301 GCATCGTGTCCACCTGTGGGCGGCGGTATTTGCCCGGACCGCCAGCCAGAACGCGAG 360  
DB 388 GCATCGTGTCCACCTGTGGGCGGCGGTATTTGCCCGGACCGCCAGCCAGAACGCGAG 447  
QY 361 TGCCAGCGTGTGCGGCGGACGCTTCTCAAGCAGACGCTTCAAGCAGTGCAG 420  
DB 448 TGCCAGCGTGTGCGGCGGACGCTTCTCAAGCAGACGCTTCAAGCAGTGCAG 507  
QY 421 CCCACCGCACTGCAAGCGGCTTGGGCTGAGCTTCAATGTGCCAGGCTTCTTCCCAT 480  
DB 508 CCCACCGCACTGCAAGCGGCTTGGGCTGAGCTTCAATGTGCCAGGCTTCTTCCCAT 567  
QY 481 GACACCGTGTGCAAGCTGTGAGCTTCCCTCAAGCAGACGAGGTACCGAGAGCTGAG 540  
DB 568 GACACCGTGTGCAAGCTGTGAGCTTCCCTCAAGCAGACGAGGTACCGAGAGCTGAG 627  
QY 541 GAGTGTGAGGCGGCTGTGAGCTTGTGAGCTTTCAGAGACATTCATCAAGAGCTG 600  
DB 628 GAGTGTGAGGCGGCTGTGAGCTTGTGAGCTTTCAGAGACATTCATCAAGAGCTG 687

QY 601 CAGCGGTGCTGCAGGCGCTCGAGGCCCCGAGGGCTGGGGTCCGACACCAAGGGCGGC 660  
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Db 688 CAACGCTGCTGCAAGCTCTGGAAAGCTCTGAGGGCTGGGGTCCCAACCAAGGGCTGGC 747  
|||  
QY 661 CGCGCGCTTTGACGCTGAAGCTGCGTCGGCGGCTCACGAGGCTCTCTGGGGGCGCAGGAC 720  
|||  
Db 748 AGGCTGCACTGCNACTGAAGCTTTCGAGAGGCTCACTGACTCTCTGGAGCTCAAGAT 807  
|||  
QY 721 GGGCGCTGCTGCTGCGGCTGCTGCAGGCGCTGCGCTGCCAGGATGCCCGGGCTGGAG 780  
|||  
Db 808 GGAGCTCTGCTGCTGAGGCTGCTGCAAGCTCTGAGGCTGCAAGGATGCCCTGGAGTGGAG 867  
|||  
QY 781 CGNAGCTGCTGAGCGCTTCTCTCCCTGTCAC 813  
|||  
Db 868 CGCTCTGAGGGAACGCTTCTGCTGTCAC 900  
|||

## RESULT 8

US-09-896-096A-3

; Sequence 3, Application US/09896096A

; Patent No. US20020061559A1

; GENERAL INFORMATION:

; APPLICANT: ASHKENAZI, AVI J

; APPLICANT: BOTSTEIN, DAVID

; APPLICANT: DODGE, KELLY H.

; APPLICANT: GURNEY, AUSTIN L.

; APPLICANT: KIM, KYUNG JIN

; APPLICANT: LAWRENCE, DAVID A.

; APPLICANT: PITTI, ROBERT

; APPLICANT: ROY, MARGARET A.

; APPLICANT: TUMAS, DANIEL B.

; APPLICANT: WOOD, WILLIAM I.

; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog

; FILE REFERENCE: P1134R2 REVISED

; CURRENT APPLICATION NUMBER: US/09/896,096A

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/157,289

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/059,288

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: US 60/094,640

; PRIOR FILING DATE: 1998-07-30

; NUMBER OF SEQ ID NOS: 18

; SEQ ID NO 3

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Unknown organism

; NAME/KEY: unsure

; LOCATION: 62, 73, 86, 98

; OTHER INFORMATION: unknown base

US-09-896-096A-3

## Query Match

Best Local Similarity 58.2%; Score 473.4; DB 10; Length 491;

Matches 485; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 101 GCCGAGACAGCCCCACGACGCTGCGCCGCTGTCCACCGCGCACTACACGAGTTCTGGA 160  
Db 1 GCCGAGACAGCCCCACGACGCTGCGCCGCTGTCCACCGCGCACTACACGAGTTCTGGA 60  
|||  
QY 161 ACTACCTGGAGCGCTGCGGCTACTGCAACGCTCTCTGCGGGAGCGTGAGGAGGAGCAC 220  
Db 61 ANTAACCTGGAGCNCCTGCGCTACTGNAACGCTCTCTGNGGGAGCGTGAGGAGGAGCAC 120  
|||  
QY 221 GGGCTTGCACGCGCACCCACACACCGTGCCTGCGCTGCCGACCGGCTTCTTCGCGACG 280  
Db 121 GGGCTTGCACGCGCACCCACACACCGTGCCTGCGCTGCCGACCGGCTTCTTCGCGACG 180  
|||  
QY 281 CTGGTTTCTGTTGGACGCGCATCGTGTCCACCTGCTGCGGCGTCAATTGCCCGGGCA 340  
|||

Db 181 CTGGTTTCTGTTGGAGACGCGATCGTGTCCACCTGCTGCGGCGGTGATTGCCCGGGCA 240  
|||  
QY 341 CCCCCAGCAGAACACGCGAGTGGC-AGCGTGTGCCCCCGGAGGACCTTCTCAGCGAGCAC 399  
|||  
Db 241 CCCCCAGCAGAACACGCGAGTGGC-AGCGTGTGCCCCCGGAGGACCTTCTCAGCGAGCAC 300  
|||  
QY 400 TCCAGCTCAGAGCAGTCCAGGCCCCACCGCAACTGCACGCGCCCTGGGCGCTTCAAT 459  
|||  
Db 301 TCCAGCTCAGAGCAGTGGCAGGCCCCACCGCAACTGCACGCGCCCTGGGCGCTTCAAT 360  
|||  
QY 460 GTCCAGGCTCTTCTCTCCCATGACACCCCTGTGCACGAGTGCACCTTCCCGCTCAGC 519  
|||  
Db 361 GTCCAGGCTCTTCTCTCCCATGACACCCCTGTGCACGAGTGCACCTTCCCGCTCAGC 420  
|||  
QY 520 ACCAGGTTACCGAGGCTGAGGAGTGTGAGCGTGTGCGGTATCGACTTTGTGGCTTCCAG 579  
|||  
Db 421 ACCAGGTTACCGAGGCTGAGGAGTGTGAGCGTGTGCGGTATCGACTTTGTGGCTTCCAG 480  
|||  
QY 580 GACATCTCCAT 590  
|||  
Db 481 GACATCTCCAT 491  
|||

## RESULT 9

US-09-894-924-3

; Sequence 3, Application US/09894924

; Patent No. US20020065210A1

; GENERAL INFORMATION:

; APPLICANT: ASHKENAZI, AVI J

; APPLICANT: BOTSTEIN, DAVID

; APPLICANT: DODGE, KELLY H.

; APPLICANT: GURNEY, AUSTIN L.

; APPLICANT: KIM, KYUNG JIN

; APPLICANT: LAWRENCE, DAVID A.

; APPLICANT: PITTI, ROBERT

; APPLICANT: ROY, MARGARET A.

; APPLICANT: TUMAS, DANIEL B.

; APPLICANT: WOOD, WILLIAM I.

; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog

; FILE REFERENCE: P1134R2 REVISED

; CURRENT APPLICATION NUMBER: US/09/894,924

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/157,289

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/059,288

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: US 60/094,640

; PRIOR FILING DATE: 1998-07-30

; NUMBER OF SEQ ID NOS: 18

; SEQ ID NO 3

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Unknown organism

; NAME/KEY: unsure

; LOCATION: 62, 73, 86, 98

; OTHER INFORMATION: unknown base

US-09-894-924-3

## Query Match

Best Local Similarity 58.2%; Score 473.4; DB 10; Length 491;

Matches 485; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 101 GCCGAGACAGCCCCACGACGCTGCGCCGCTGTCCACCGCGCACTACACGAGTTCTGGA 160  
Db 1 GCCGAGACAGCCCCACGACGCTGCGCCGCTGTCCACCGCGCACTACACGAGTTCTGGA 60  
|||  
QY 161 ACTACCTGGAGCGCTGCGGCTACTGCAACGCTCTCTGCGGGAGCGTGAGGAGGAGCAC 220  
Db 61 ANTAACCTGGAGCNCCTGCGCTACTGNAACGCTCTCTGNGGGAGCGTGAGGAGGAGCAC 120  
|||  
QY 221 GGGCTTGCACGCGCACCCACACACCGTGCCTGCGGCTGCCGACCGGCTTCTTCGCGACG 280  
|||

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Db 121 GGGCTTCCAGCAGCACCACCAACCGTGTGCGCTGCGCCGACCGCGGCTTCTTCCGCGACG 180
Qy 281 CTGATTTCTGCTTGGAGAGAGCATGATGTCACCTGATGCGCGGATATTGGCCCCGGGCA 340
Db 181 CTGATTTCTGCTTGGAGAGAGCATGATGTCACCTGATGCGCGGATATTGGCCCCGGGCA 240
Qy 341 CCCCCCAGCAAGAACCCAGATGCC-AGCCGTGCCCCCAGGACCTTCTCAGCAGCAGC 399
Db 241 CCCCCCAGCAAGAACCCAGATGCCAGTACCGGTGCCCCCAGGACCTTCTCAGCAGCAGC 300
Qy 400 TCCAGCTCAAGAGAGTCCAGCCCGACCGCAACTGCAAGCGCCCTTGGGCTTGCCTCAAT 459
Db 301 TCCAGCTCAAGAGAGTCCAGCCCGACCGCAACTGCAAGCGCCCTTGGGCTTGCCTCAAT 360
Qy 460 GTGCGAGGCTTCTCTCCATGACACCTGTCGACCAAGCTGCACTGAGCTTCCCTCAGC 519
Db 361 GTGCGAGGCTTCTCTCCATGACACCTGTCGACCAAGCTGCACTGAGCTTCCCTCAGC 420
Qy 520 ACCAGGATACAGAGAGTGAAGAGTGAAGCGTGCCTCATGCACTTGTGCTTCCAG 579
Db 421 ACCAGGATACAGAGAGTGAAGAGTGAAGCGTGCCTCATGCACTTGTGCTTCCAG 480
Qy 580 GACATCTCCAT 590
Db 481 GACATCTCCAT 491
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RESULT 10
US-09-877-156-7
; Sequence 7, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 459
; TYPE: DNA
; ORGANISM: human
US-09-877-156-7
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Query Match 56.5%; Score 459; DB 10; Length 459;
Best Local Similarity 100.0%; Pred. No. 7,8e-88;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 166 CTGAGAGCGTGGCGCTACTGCAAGCTCTGTGCGGAGCGTGAAGAGAGGACGGGCT 225
Db 1 CTGAGAGCGTGGCGCTACTGCAAGCTCTGTGCGGAGCGTGAAGAGAGGACGGGCT 60
Qy 226 TGGCAGCCCAACCAACCAACCGTCTGCGGCAACCGGCTTCTTGGGCAAGCTGCT 285
Db 61 TGGCAGCCCAACCAACCAACCGTCTGCGGCAACCGGCTTCTTGGGCAAGCTGCT 120
Qy 286 TTTGCTTGGAGAGAGCATGCTGTCACCTGATGTCGCGGCTGATTTGCCCGGAGACCC 345
Db 121 TTTGCTTGGAGAGAGCATGCTGTCACCTGATGTCGCGGCTGATTTGCCCGGAGACCC 180
Qy 346 AGCCAGAAACAGAGTCCAGCGGTGCCCCCAGGACCTTTCTCAGCAGCTCCAGC 405
Db 181 AGCCAGAAACAGAGTCCAGCGGTGCCCCCAGGACCTTTCTCAGCAGCTCCAGC 240
Qy 406 TCGAGAGAGTCCAGCGGCAACCGCAACTGCAAGCGGCTTGGGCTTGGGCTTCAATGTC 465
Db 241 TCGAGAGAGTCCAGCGGCAACCGCAACTGCAAGCGGCTTGGGCTTGGGCTTCAATGTC 300
Qy 466 GGCTTCTCTCCATGACACCTGTGCAACGAGTGCATGCTGCTTCCCTCAGACACGAG 525
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Db 301 GGGCTTCTCCATGACACCTGTGTCACAGCTGCATGAGCTTCCCTCAGACACGAG 360
Qy 526 GTACACAGAGCTAGAGAGTGTAGAGCTGCGGCTATGACTTTGTGCTTCCAGACATC 585
Db 361 GTACACAGAGCTAGAGAGTGTAGAGCTGCGGCTATGACTTTGTGCTTCCAGACATC 420
Qy 586 TCCATCAAGAGCTGAGAGCGGCTGTGTCAGAGCCCTCGAG 624
Db 421 TCCATCAAGAGCTGAGAGCGGCTGTGTCAGAGCCCTCGAG 459
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RESULT 11
US-09-935-727-33
; Sequence 33, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon optimized TNFR-6 alpha
US-09-935-727-33
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Query Match 48.2%; Score 392.2; DB 10; Length 1550;
Best Local Similarity 67.7%; Pred. No. 8,6e-74;
Matches 550; Conservative 0; Mismatches 263; Indels 0; Gaps 0;
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Qy 1 GTGGCAAGAAACACCAACCTTATCCCTGCGGAGACGACAGAGACGGGAGGGCTGCTGTC 60
Db 738 GTTGTGTAAGAACACCAACCTTATCCCTGCGGAGACGACAGAGACGGGAGGGCTGCTGTC 797
Qy 61 GCCCATGCCCCCAGGACCTTTGTGACGCGCCGTGCGCGGAGACAGCCCAAGAGC 120
Db 798 GCTCATATGTCACACCAAGTACTTTGTTCAAAAGCATGTGAAGAGATTCTCAACTACT 857
Qy 121 TGTGCGCGGCTGTACCGGCACTACAGCAGTTTGTGAATCTACTGAGAGGCTGCC 180
Db 858 TGTGCTTCATGTCACCAAGACATTACCTCAATTTTGAAGTACTGGAAGATGTACA 917
Qy 181 TACTGAAGATGCTCTGCGGAGAGCTGAGAGAGGACAGGCGCTTGCAACGACACCAAC 240
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; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)..(582)
US-09-935-727-3

Query Match          47.7%; Score 387.4; DB 10; Length 1667;
Best Local Similarity 79.6%; Pred. No. 8,8e-73;
Matches 534; Conservative 0; Mismatches 1; Indels 136; Gaps 1;

QY 1 GTGCGAGAAACACCCACCTACCTCCCTGGGGGACGCGAGACAGAGAGGAGCGGCTGGTGTC 60
Db 160 GTGCGAGAAACACCCACCTACCTCCCTGGGGGACGCGAGACAGAGAGGAGCGGCTGGTGTC 219
QY 61 GCCAGTGGCCCCAGGACACCTTTGTGACGCGCGCTGCGCGGAGACAGCCACCGACG 120
Db 220 GCCAGTGGCCCCAGGACACCTTTGTGACGCGCGCTGCGCGGAGACAGCCACCGACG 279
QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGACAGTCTTGGAACTTACCTGGAGCGCTGCCGC 180
Db 280 TGTGGCCCGTGTCCACCGCGCCACTACACGACAGTCTTGGAACTTACCTGGAGCGCTGCCGC 339
QY 181 TACTGCAACGTCTCTTGGGGGAGCGTGGAGGAGGACGCGGCTTGCACACGCCAC 240
Db 340 TACTGCAACGTCTCTTGGGGGAGCGTGGAGGAGGACGCGGCTTGCACACGCCAC 399
QY 241 AACCTGCGCTCGCGCTGCCGACCGGCTTCTTCCGACGCTGCTTCTGCTTGGAGCAC 300
Db 400 AACCTGCGCTCGCGCTGCCGACCGGCTTCTTCCGACGCTGCTTCTGCTTGGAGCAC 459
QY 301 GCATCGTGTCCACCTGCTGCGCGCTGATTTGCCCGC----- 336
Db 460 GCATCGTGTCCACCTGCTGCGCGCTGATTTGCCCGCGGTGATTTGCCCGCGGAGGG 519
QY 337 ----- 336
Db 520 GCCCCAGGAGTGGTGGCCGAGGTGTGGCAGGGGTGAGGTTGCTGCTCCAGCCTTGCA 579
QY 337 -----GGCACCCC 344
Db 580 CCTGAGCTAGGACACAGATTCCCTGACCCCTGTTCTTCCCTCTGCTGCGACGGCACCCC 639
QY 345 CAGCCAGAACACACGAGTGGCAGCGCTGCCCGCCAGCACCTTCTCAGCCAGCAGCTCCAG 404
Db 640 CAGCCAGAACACGAGTGGCAGCGCTGCCCGCCAGCACCTTCTCAGCCAGCAGCTCCAG 699
QY 405 CTGAGAGCAGTGCACGCCGCCACCGCAACTGACGGCCCTGGGCTGCTCAATGTGCC 464
Db 700 CTGAGAGCAGTGCACGCCGCCACCGCAACTGACGGCCCTGGGCTGCTCAATGTGCC 759
QY 465 AGGCTCTTCTCCCATGACACCTGTGACCCAGCTGACCTGCTCCCTCAGCAGCCAG 524
Db 760 AGGCTCTTCTCCCATGACACCTGTGACCCAGCTGACCTGCTCCCTCAGCAGCCAG 819
QY 525 GGTACCCAGGAG 535
Db 820 GGTACCCAGGAG 830

RESULT 13
US-09-935-727-28
; Sequence 28, Application US/09935727
; Patent No. US20020150583A1
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; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)..(582)
US-09-935-727-3

Query Match          47.7%; Score 387.4; DB 10; Length 1667;
Best Local Similarity 79.6%; Pred. No. 8,8e-73;
Matches 534; Conservative 0; Mismatches 1; Indels 136; Gaps 1;

QY 1 GTGCGAGAAACACCCACCTACCTCCCTGGGGGACGCGAGACAGAGAGGAGCGGCTGGTGTC 60
Db 160 GTGCGAGAAACACCCACCTACCTCCCTGGGGGACGCGAGACAGAGAGGAGCGGCTGGTGTC 219
QY 61 GCCAGTGGCCCCAGGACACCTTTGTGACGCGCGCTGCGCGGAGACAGCCACCGACG 120
Db 220 GCCAGTGGCCCCAGGACACCTTTGTGACGCGCGCTGCGCGGAGACAGCCACCGACG 279
QY 121 TGTGGCCCGTGTCCACCGCGCCACTACACGACAGTCTTGGAACTTACCTGGAGCGCTGCCGC 180
Db 280 TGTGGCCCGTGTCCACCGCGCCACTACACGACAGTCTTGGAACTTACCTGGAGCGCTGCCGC 339
QY 181 TACTGCAACGTCTCTTGGGGGAGCGTGGAGGAGGACGCGGCTTGCACACGCCAC 240
Db 340 TACTGCAACGTCTCTTGGGGGAGCGTGGAGGAGGACGCGGCTTGCACACGCCAC 399
QY 241 AACCTGCGCTCGCGCTGCCGACCGGCTTCTTCCGACGCTGCTTCTGCTTGGAGCAC 300
Db 400 AACCTGCGCTCGCGCTGCCGACCGGCTTCTTCCGACGCTGCTTCTGCTTGGAGCAC 459
QY 301 GCATCGTGTCCACCTGCTGCGCGCTGATTTGCCCGC----- 336
Db 460 GCATCGTGTCCACCTGCTGCGCGCTGATTTGCCCGCGGTGATTTGCCCGCGGAGGG 519
QY 337 ----- 336
Db 520 GCCCCAGGAGTGGTGGCCGAGGTGTGGCAGGGGTGAGGTTGCTGCTCCAGCCTTGCA 579
QY 337 -----GGCACCCC 344
Db 580 CCTGAGCTAGGACACAGATTCCCTGACCCCTGTTCTTCCCTCTGCTGCGACGGCACCCC 639
QY 345 CAGCCAGAACACACGAGTGGCAGCGCTGCCCGCCAGCACCTTCTCAGCCAGCAGCTCCAG 404
Db 640 CAGCCAGAACACGAGTGGCAGCGCTGCCCGCCAGCACCTTCTCAGCCAGCAGCTCCAG 699
QY 405 CTGAGAGCAGTGCACGCCGCCACCGCAACTGACGGCCCTGGGCTGCTCAATGTGCC 464
Db 700 CTGAGAGCAGTGCACGCCGCCACCGCAACTGACGGCCCTGGGCTGCTCAATGTGCC 759
QY 465 AGGCTCTTCTCCCATGACACCTGTGACCCAGCTGACCTGCTCCCTCAGCAGCCAG 524
Db 760 AGGCTCTTCTCCCATGACACCTGTGACCCAGCTGACCTGCTCCCTCAGCAGCCAG 819
QY 525 GGTACCCAGGAG 535
Db 820 GGTACCCAGGAG 830

RESULT 13
US-09-935-727-28
; Sequence 28, Application US/09935727
; Patent No. US20020150583A1
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: P454P2
CURRENT APPLICATION NUMBER: US/09/935,727
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 09/518,931
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/168,235
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/146,371
PRIOR FILING DATE: 1999-08-02
PRIOR APPLICATION NUMBER: 60/131,964
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/131,270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/124,092
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/121,774
PRIOR FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: 09/006,352
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/035,496
PRIOR FILING DATE: 1997-01-14
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 1796
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Intron
LOCATION: 425-560
NAME/KEY: Intron
LOCATION: 756-1512
US-09-935-727-28

Query Match          47.6%; Score 387; DB 10; Length 1796;
Best Local Similarity 79.4%; Pred. No. 1,1e-72;
Matches 533; Conservative 1; Mismatches 1; Indels 136; Gaps 1;
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Qy 345 CAGCCAGAACAGCAGTGTGCGAGCGTGTGCGCGAGCAGCTTCTGACGACGCTTCAG 404
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Qy 465 AGGCTTCTCTCCATGACACCTGTGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 524
Db 688 AGGCTTCTCTCCATGACACCTGTGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
Qy 525 GGTACGAGAG 535
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RESULT 14
US-09-896-096A-5
Sequence 5, Application US/09896096A
Patent No. US2002006159A1
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GENERAL INFORMATION:
APPLICANT: ASHERNAZI, AVI J
APPLICANT: BOTSTEIN, DAVID
APPLICANT: DODGE, KELLY H.
APPLICANT: GURNEY, AUSTIN L.
APPLICANT: KIM, KYUNG JIN
APPLICANT: LAWRENCE, DAVID A.
APPLICANT: PITT, ROBERT
APPLICANT: ROY, MARGARET A.
APPLICANT: TUMAS, DANIEL B.
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: DCR3 polypeptide, A TNFR Homolog
FILE REFERENCE: P134R2 REVISED
CURRENT APPLICATION NUMBER: US/09/896,096A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 09/157,289
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/059,288
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: US 60/094,640
PRIOR FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 5
LENGTH: 271
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Unknown organism
NAME/KEY: unsure
LOCATION: 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233
OTHER INFORMATION: unknown base
US-09-896-096A-5
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Query Match          30.2%; Score 245.2; DB 10; Length 271;
Best Local Similarity 92.3%; Pred. No. 3.8e-43;
Matches 250; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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## RESULT 15

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US-09-894-924-5
; Sequence 5, Application US/09894924
; Patent No. US20020065210A1
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/894,924
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 5
; LENGTH: 271
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Unknown organism
; NAME/KEY: unsure
; LOCATION: 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233
; OTHER INFORMATION: unknown base
US-09-894-924-5
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Query Match 30.2%; Score 245.2; DB 10; Length 271;
Best Local Similarity 92.3%; Pred. No. 3.8e-43;
Matches 250; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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Qy 281 CTGGTTTCTGCTTGGAGCAGCATCGTGTCCACTGGTGCAGCGGTGATTGCCCGGGCA 340
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Db 241 CCCCAGCCAGACAGCATGCAAGCCGTG 271
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Search completed: January 6, 2003, 16:08:07  
Job time : 63 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2003, 11:21:41 ; Search time 2905 Seconds  
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2714.926 Million cell updates/sec

Title: US-09-936-024-1  
Sequence: 1 VAETPTYPWMDAETGERLYC.....RVARMGELERSVERFLPVH 271

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 2054640 seqs, 14551402878 residues  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09936024 @CGN 1.1 2425 @runat\_06012003.11607.12130 -NCPU=6 -ICPU=3  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb\_hcg:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
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10: gb\_ro:\*  
11: gb\_sts:\*  
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15: em\_ba:\*  
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17: em\_hum:\*  
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29: em\_vi:\*  
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32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
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35: em\_hcg\_rtd:\*  
36: em\_hcg\_mam:\*  
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41: em\_hcgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1491	100.0	813	6 AX119833	AX119833 Sequence
2	1491	100.0	813	6 AX167223	AX167223 Sequence
3	1491	100.0	813	6 AX375169	AX375169 Sequence
4	1491	100.0	903	9 AF134240	AF134240 Homo sapi
5	1491	100.0	1048	9 AF217794	AF217794 Homo sapi
6	1491	100.0	1055	6 AX082868	AX082868 Sequence
7	1491	100.0	1114	6 AX055373	AX055373 Sequence
8	1491	100.0	1114	6 AX056645	AX056645 Sequence
9	1491	100.0	1114	9 AF104419	AF104419 Homo sapi
10	1491	100.0	1125	9 BC017065	BC017065 Homo sapi
11	1491	100.0	1150	6 BC034349	BC034349 Homo sapi
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13	1491	100.0	1347	6 AF171895	AF171895 Sequence
14	1491	100.0	1428	9 AF217793	AF217793 Homo sapi
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21	1476	99.0	936	6 AX167230	AX167230 Sequence
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26	841	56.4	459	6 AR171887	AR171887 Sequence
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37	440.5	29.5	2139	6 AX202074	AX202074 Sequence
38	436.5	29.3	1356	6 AX076608	AX076608 Sequence
39	433	28.0	525	6 AR099131	AR099131 Sequence
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RESULT 1

## ALIGNMENTS

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LOCUS          Sequence 2 from Patent WO0128582.
DEFINITION
ACCESSION      AX119833
VERSION        AX119833.1  GI:14036593
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 813)
AUTHORS       Bumol,T.F. and Cohen,F.J.
TITLE         Therapeutic applications of flint polypeptides
JOURNAL       Patent: WO 0128582-A 2 26-APR-2001;
              ELI LILLY AND COMPANY (US)
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  source       1..813
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BASE COUNT    122 a 298 c 267 g 126 t
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QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
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QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
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QY 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
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QY 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleCysArgLeu 200
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QY 241 GlyAlaLeuValArgLeuLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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QY 261 ArgSerValArgGluArgPheLeuProValHis 271
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RESULT 2
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LOCUS          Sequence 2 from Patent WO0142463.
DEFINITION
ACCESSION      AX167223
VERSION        AX167223.1  GI:14596692
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 813)
AUTHORS       Lu,J. and Witcher,D.R.
TITLE         Improving stability of flint through o-linked glycosylation
JOURNAL       Patent: WO 0142463-A 2 14-JUN-2001;
              ELI LILLY AND COMPANY (US)
FEATURES
  source       1..813
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
BASE COUNT    122 a 298 c 267 g 126 t
ORIGIN
Alignment Scores:
Pred. No.:    3.84e-64      Length:      813
Score:        1491.00      Matches:    271
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:  100.00%      Indels:     0
DB:           6      Gaps:      0
US-09-936-024-1 (1-271) x AX167223 (1-813)

QY 1 ValAlaGluThrProThyProTrpArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 1 GTGGCAGAAACACCCACTACCCCTGGCGGACGACGAGACAGGGAGCGGTGGTGC 60

QY 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 61 GCCCATGTGCCCCCAGCACCTTTGTGACGGCGCTGTGCGCGACAGACGCCACGACG 120

QY 41 CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg 60
Db 121 TGTGGCCCGTGTCCACCGGCCACTACACGAGTTCTTGGAACTACCTGGAGCGCTGCCG 180

QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80
Db 181 TACTGCAACGTCTCTGCGGGAGCGTGAGGAGGAGGACGGGCTTGCACGCCACCCAC 240

QY 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 241 AACCGTGCTGCGCGTCCCGCACCGGCTTCTTCCGACAGCTGGTTCTGCTTGGAGCAC 300

QY 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 301 GCATCGTGTCCACCTGCTGCGCGCGTGTATGTCGCCGCGGACCGGCTTGCAGCAGTGC 360

QY 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerSerSerSerSerSerSer 140
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Db 361 TGCCAGCGCTGCCCCCGACGACCTTCTCAGCCAGCAGCTCAGCTCAGAGAGTGCAG 420

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Db 421 CCCACCGCAACTGCACCGCCCTGGCGCTGCCTCAATGTGCCAGGCTCTTCTCCCAT 480

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Qy 221 ArgAla1aleuGlnLeuLysLeuArgArgArgLeuThrgLuleuGlyValaGlnaSp 240

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Qy 241 GlnAla1aleuLeuValaArgLeuLeuGlnAlaleuArgVala1aArgMetProGlyLeuGlu 260

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RESULT 3

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LOCUS AX375169 Sequence 2 from Patent WO0209668.

DEFINITION AX375169

ACCESSION AX375169

VERSION AX375169.1 GI:19169920

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Micanovic, R. and Wilcher, D.R.

TITLE Pulmonary administration of flint

JOURNAL Patent: WO 0209668-A 2 07-FEB-2002;

ELI Lilly AND COMPANY (US)

FEATURES

source 1..813

location/Qualifiers

BASE COUNT 122 a 298 c 267 g 126 t

ORIGIN

Alignment Scores:

Pred. No.: 3 84e-64 Length: 813

Score: 1491.00 Matches: 271

Percent Similarity: 100.00% Conservatave: 0

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US-09-936-024-1 (1-271) x AX375169 (1-813)

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Qy 41 CysGlyProCySPProProArgHisTyThrgLInPheTrpaNtyLeuGluArgCyAsArg 60

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Qy 61 TyrcysaenValleuCySegLyuArgLugLulaArgAlaCySHisa1aThHis 80

Db 181 TACTGCAACGCTCTGTGCGGGAGCGTGAAGAGAGCAGAGGCTTGCCACCGCACCCAC 240

Qy 81 AsnArg1aCySArgCySArgThrgLyphePheAlaHisa1aGlyPheCySLeuGluHis 100

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Qy 121 CysGlnProCySPProProGlyThraPheSerAlaSerSerSerSerGlnGlyGln 140

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Db 481 GACACCTGTGTGCACACAGTGTGACTTCCCTCCACACACAGGATGCCAGAGCTGAG 540

Qy 181 GluCySegLuarGalaVal11leAspPheVal11aPheGlnaAsp11eSer11eLysArgLeu 200

Db 541 GAGTGTAGGCTGCGCTGCATGCATTTGTGCTTCCAGACATCTTCATCAAGAGCTG 600

Qy 201 GlnArgLeuLeuGlnAlaleuGlnAlaProGlyLgLYTPGlyProThraArgValaGly 220

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Qy 221 ArgAla1aleuGlnLeuLysLeuArgArgArgLeuThrgLuleuGlyValaGlnaSp 240

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Qy 241 GlnAla1aleuLeuValaArgLeuLeuGlnAlaleuArgVala1aArgMetProGlyLeuGlu 260

Db 721 GGGCGCTGTGTGTGCGGCTGCTGCAGGCGCTGCGCTGCGCAGGATGCCGGGCTGAG 780

Qy 261 ArgSerValaArgGluArgPheLeuProValHis 271

Db 781 CGGAGCGTCCGTGAGCGCTTCTCCTGTGCAC 813

RESULT 4

AF134240 903 bp mRNA linear PRI 11-MAY-1999

LOCUS AF134240

DEFINITION Homo sapiens tumor necrosis factor receptor homolog (TR6) mRNA, complete cds.

ACCESSION AF134240

VERSION AF134240.1 GI:4768938

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Yu, K.Y., Kwon, B., Ni, J., Zhai, Y., Ebner, R. and Kwon, B.S.

TITLE A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis

JOURNAL J. Biol. Chem. 274 (20), 13733-13736 (1999)

REFERENCE 2

AUTHORS Kwon, B.S. and Yu, K.Y.

TITLE Direct Submission

JOURNAL Submitted (10-MAR-1999) Micro/ImmunoI, Indiana University, 635 Barnhill Drive, Indianapolis, IN 46202, USA

FEATURES

source 1..903

location/Qualifiers





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Qy 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 934 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 966

RESULT 7
AX055373
LOCUS AX055373 1114 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 3 from Patent WO073452.
ACCESSION AX055373
VERSION AX055373.1 GI:12228659
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1114)
REFERENCE
AUTHORS Ashkenazi,A.J., Baker,K.P., Chan,B., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hebert,C., Henzel,W., Kabakoff,R.C., Shelton,D.L.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0073452-A 3 07-DEC-2000;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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Alignment Scores:
Pred. No.: 5.28e-64 Length: 1114
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db 248 GCCAGTGGCCCCAGGACCTTTGTGAGCGCGCTGCGCGGACAGCCCCACGACG 307
Qy 41 CysGlyProCysProProArgHisTyrThrGlnPheThrAsnTyrLeuGluArgCysArg 60
Db 308 TGTGGCCCGTGTCCACCGCGCCACCTACACGAGTCTTGGAACTCTGGAGCGCTGCCGC 367
Qy 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 368 TACTGCAACGTCTCTGCGGGGAGCGTGAGAGGAGGAGCGGCTTGCCACGCCACCCAC 427
Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 428 AACCGTGCTCGCGTGGCGCACCGGCTTTCTTGGCGACGCTGGTTCTTCTTGGAGCAC 487
Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
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Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGlu 180
Db 668 GACACCTGTGCACGAGCTGCACCTGGCTTCCCTCCAGCCAGGTTACAGAGCTGAG 727
Qy 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
Db 728 GAGTGTGAGCGTGGCGCTCATCGACTTTGGCTTTTCCAGGACATCTCCATCAGAGGCTG 787
Qy 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaGly 220
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Qy 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 968 CGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC 1000

RESULT 8
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LOCUS AX056645 1114 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 1 from Patent WO0075316.
ACCESSION AX056645
VERSION AX056645.1 GI:12309639
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1114)
REFERENCE
AUTHORS Ashkenazi,A.J., Goddard,A., Gurney,A.L., Hillan,K., Napier,M. and
Wood,W.I.
TITLE Methods and compositions for inhibiting neoplastic cell growth
JOURNAL Patent: WO 0075316-A 1 14-DEC-2000;
Genentech, Inc. (US)
FEATURES
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/organism="Homo sapiens"
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BASE COUNT 188 a 379 c 356 g 191 t
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Alignment Scores:
Pred. No.: 5.28e-64 Length: 1114
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Qy 41 CysGlyProCysProProArgHisTyrThrGlnPheThrAsnTyrLeuGluArgCysArg 60
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Db 428 AACGTGCTCCCGCTGTGCGGACCGGCTTCTTCCGCGACCGCTGTTCTGCTTGGAGCAC 487
Qy 101 AlaserCySPProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 488 GCATCGTGTCCACCTGGTGGCGGCGCTGATTGCCCGCGGACCCCGACAGAACACGACG 547
Qy 121 CyAGlnProCySPProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCyAGln 140
Db 548 TGCACGCGGTGCCCCCGAGGACCTTCTCAGCCAGACAGCTCAGCTCAGAGAGTGCAG 607
Qy 141 ProHisArgAsnCySPThraAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
Db 608 CCCACCGCAACTGCACGCGCTGGGCTGGGCTGCTCATGTGCCAGGCTTCTTCCCAT 667
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Db 668 GACACCTGTGCACACGAGTGCAGTGGCTTCCCTCAGACACAGGAGTACAGAGAGTGCAG 727
Qy 181 GluCyAGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLeuArgLeu 200
Db 728 GAGGTGAGCGTCCGCTGATGACTTGTGGCTTCCAGGACATCTTCATCAAGAGGCTG 787
Qy 201 GlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTPGlyProThrProArgAlaGly 220
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Qy 221 ArgAlaAlaLeuGlnLeuLeuLeuArgArgArgLeuThrGluLeuGlyAlaGlnAsp 240
Db 848 CGCGCGGCTTGCAGCTGAACTGCTGGTGGCGGCTCAGGAGCTCTGGGGCGGAGAGC 907
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Qy 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 968 CGAGCGCTCCGTCGAGCGCTTCTCTCTGTGCAC 1000

RESULT 9
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LOCUS Homo sapiens decoy receptor 3 (Dcr3) mRNA, complete cds.
DEFINITION AF104419
ACCESSION AF104419.1 GI:4106877
VERSION AF104419.1
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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1 (bases 1 to 1114)
Plitt,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
Gadowski,P.J., Wood,W.I., Gurney,A.L., Hillan,K.J., Cohen,R.L.,
Goddard,A.D., Botstein,D. and Ashkenazi,A.
Genomic amplification of a decoy receptor for Fas ligand in lung
and colon cancer
Nature 396 (6712), 699-703 (1998)
JOURNAL MEDLINE 99087326
PUBMED 9872321
AUTHORS Plitt,R.M., Marsters,S.A., Lawrence,D.A., Roy,M., Kischkel,F.C.,
Dowd,P., Huang,A., Donahue,C.J., Sherwood,S.W., Baldwin,D.T.,
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Goddard,A.D., Botstein,D. and Ashkenazi,A.

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TITLE Direct Submission
JOURNAL Submitted (04-NOV-1998) Molecular Oncology, Genentech, 1 DNA Way,
San Francisco, CA 94080, USA
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BASE COUNT 188 a 379 c 356 g 191 t
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Alignment Scores:
Pred. No.: 5.28e-64 Length: 1114
Score: 1491.00 Matches: 271
Percent Similarity: 100.00% Conservative: 0
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Qy 181 GluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArgLeu 200
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Db 788 CAGCGCTCTCTCAGCGCTTCAGGCGCCGAGGGCTGGGTCGCGACACCAAGGCGGCG 847
Qy 221 ArgAlaLeuGlnLeuLysLeuArgArgLeuThrGluLeuLeuGlyAlaGlnAsp 240
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Qy 241 GlyAlaLeuLeuValArgLeuGlnAlaLeuArgValAlaArgMetProGlyLeuGlu 260
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Qy 261 ArgSerValArgGluArgPheLeuProValHis 271
Db 968 CGAGGCTCCGTGAGGCTCTCTCCCTGTGCAC 1000

RESULT 10
LOCUS BC017065 1125 bp mRNA linear PRI 09-NOV-2001
DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member
6b, decoy, clone MGC:9587 IMAGE:3886635, mRNA, complete cds.
ACCESSION BC017065
VERSION BC017065.1 GI:16877637
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1125)
Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DPF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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BASE COUNT 200 a 378 c 356 g 191 t
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Alignment Scores: 5,34e-64 Length: 1125
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Score: 1491.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
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Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
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QY 241 G1A1A1euleuValArg1euleuG1A1A1euleuArgVal1A1ArgMetProG1YleuGlu 260  
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RESULT 11  
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DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member 6b, decoy, clone MGC:21079 IMAGE:4752507, mRNA, complete cds.  
ACCESSION BC034349  
VERSION BC034349.1 GI:21706464  
KEYWORDS MGC.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1150)  
Strausberg, R.  
Direct Submission  
Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-rt@mail.nih.gov](mailto:cgabs-rt@mail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-MGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowals, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richarde, S., Gibbs, R.A.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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ORIGIN

Alignment Scores:  
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US-09-936-024-1 (1-271) x BC034349 (1-1150)

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QY 61 TyrCysAnVal1euleuValArgGluGluGluGluGluGluGluGluGluGluGluGlu 80  
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Db 976 CGGAGCGTCCGTGAGCGCTTCCCTGTCAC 1008

RESULT 12  
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LOCUS AX017828 1168 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 1 from Patent WO9946376.  
ACCESSION AX017828  
VERSION AX017828.1 GI:10042431  
KEYWORDS



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Oy	221	ArgAlaalaleuGlNleuLytleuXrgrArgAgleuThngluLeuLgylalaGlasp	240
Db	1065	CGCGGGCTTTCACCTAAAGCTGGCTGGCGCGCTCACGGAGCTTCTGGGGCGGAGAAC	1124
Oy	241	GlYalaLeuValArjArgleuGlNalaLeuArxValalAargMetProglyLeuGl	260
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DEFINITION	Homo sapiens M68C mRNA, alternatively spliced, complete cds.		
ACCESSION	AF217793		
VERSION	AF217793.1	GI:6969260	
KEYWORDS	.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1428) Baï,C., Connolly,B., Metzker,M.L., Hilliard,C.A., Liu,X., Sandig,V., Soderman,A., Galloway,S.M., Liu,Q., Austri,C.P. and Cabekey,C.T. Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1230-1235 (2000)		
AUTHORS	JOURNAL MEDLINE PUBMED 10655513 2 (bases 1 to 1428) Baï,C. Direct Submission Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories, Summeytown Pike, West Point, PA 19403, USA Location/Qualifiers 1..1428 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="20" /map="20q13.3" /cell_type="germ cell tumor" 435..1337 /note="TNFR, decoy receptor; DCR3; alternatively spliced"		
FEATURES	JOURNAL MEDLINE PUBMED 10655513 2 (bases 1 to 1428) Baï,C. Direct Submission Submitted (21-DEC-1999) WP26A-1000, Merck Research Laboratories, Summeytown Pike, West Point, PA 19403, USA Location/Qualifiers 1..1428 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="20" /map="20q13.3" /cell_type="germ cell tumor" 435..1337 /note="TNFR, decoy receptor; DCR3; alternatively spliced"		
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Percent Similarity: 100.00% Conservative: 0  
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QY 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80  
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QY 261 ArgSerValArgGluArgPheLeuProValHis 271  
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Search completed: January 6, 2003, 12:52:56

Tue Jan. 7 08:40:16 2003

us-09-936-024-1.p2n.rge

Page 13

Job time : 2909 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 6, 2003, 11:15:33 ; Search time 73 Seconds  
(without alignments)  
764.915 Million cell updates/sec

Title: US-09-936-024-1  
Perfect score: 1491  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	499.5	33.5	285	13	Q90W71	Q90W71 oncorhynchu
2	486.5	32.6	285	13	Q90Y86	Q90Y86 oncorhynchu
3	395	26.5	302	13	Q9PUS0	Q9PUS0 salvelinus
4	333.5	22.4	459	11	Q62327	Q62327 mus musculus
5	327	21.9	482	11	O88734	O88734 mus musculus
6	313.5	21.0	433	11	O912M6	O912M6 ratu
7	287	19.2	651	13	Q98SM6	Q98SM6 gallus gall
8	275	18.4	348	12	O57103	O57103 monkeypox v
9	275	18.4	348	12	O57108	O57108 monkeypox v
10	270.5	18.1	349	12	O57100	O57100 monkeypox v
11	268.5	18.0	349	12	O57101	O57101 monkeypox v
12	268.5	18.0	349	12	O57102	O57102 monkeypox v
13	268.5	18.0	349	12	O57291	O57291 monkeypox v
14	267.5	17.9	349	12	O57099	O57099 monkeypox v
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17	260	17.4	348	12	Q85407	Q85407 variola vir
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19	260	17.4	349	12	O57111	O57111 variola vir
20	260	17.4	349	12	Q89098	Q89098 variola vir
21	260	17.4	349	12	O89118	O89118 variola vir
22	260	17.4	350	12	O57116	O57116 cowpox viru
23	259	17.4	360	12	O57118	O57118 cowpox viru
24	258.5	17.3	355	12	O85308	O85308 cowpox viru
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31	253.5	17.0	349	12	O57097	O57097 camel
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42	219.5	14.7	277	6	Q8WMO2	Q8WMO2 ovis aries
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44	202	13.5	132	13	Q90Y18	Q90Y18 salvelinus
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#### ALIGNMENTS

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DE Putative decoy receptor 3 protein.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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OC Proteocephale; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEAD KIDNEY;  
RA Pleguezuelos O., Secombes C.J.;  
RT "Screening a rainbow trout (Oncorhynchus mykiss) cDNA library."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ15137; CAC43329.1; -  
DR InterPro; IPR000561; EGF-like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3\_  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 1.  
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Matches 99; Conservativity 41; Mismatches 116; Indels 11; Gaps 4;

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DB 26 AHPPTTYWRDADGDSLTCDLCAFGYTLKHKTRKSDGCPKSHYIEMYLEKCY 85  
QY 62 CNVLGRREREARCATHNRAACRCRTGPFNAAGFCLEHASCPSGAGVIAFGTSPONTQC 121





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RP SEQUENCE FROM N.A.
RC STRAIN=NOD;
RX MEDLINE=95178848; PubMed=7872884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
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RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfreflb.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF000208; TNFR_c6; 4.
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DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KM Receptor.
FT NON_TER 1 1 S -> T.
FT VARIANT 87 87 T -> I.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 S -> F.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
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   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 213 PLD---QEGPQSPQPSILTSL-----GSTPIIEOSTKGISLPIGLIVGVTSL----- 257
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 241 GALLVRLQLA---RVAMPGLERSVRERFLP 269
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 258 GLMLGLVNCFTLVQRKKKPSCLQRDAKVPHPV 290
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 5
088734 PRELIMINARY; PRT; 482 AA.
AC 088734;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE p80 TNF-alpha receptor.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98414512; PubMed=9740674;
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Iazo P.S.;
RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
   and Characterization of the two Transcripts.";
RL Genomics 52:79-98(1998).
DR EMBL; Y14619; CAA74969.1; -.
DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.
DR EMBL; Y14622; CAA74969.1; JOINED.

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DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14679; CAA74969.1; JOINED.
DR HSSP; P19438; INCF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF000208; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KM Receptor.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FFB3C CRC64;

Query Match 21.9%; Score 327; DB 11; Length 482;
Best Local Similarity 29.3%; Pred. No. 1.2e-20;
Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;

QY 17 RLVAOCPPGTGVORPCRR-----DSPTTGCPPRHYTQFWNYLERGYCNVLGGER 69
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 52 QMCCAKCPGQYVAKHFNCKNTSDTVACADCEASMTYQVWNOFRFTCLSCSSCSTD 111
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 70 EEBARACHATHNACRCRTGPF---AHAGF---CLEHASCPCGAGVIAPGTPSONTOCC 122
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 112 QVETRACTQONNVACAGEAGRYCALKTHSGSCRCQMRLSKCGPGFVASSRAENGVLCK 171
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 123 PCPPGTFASSSSEOCQPHRNCTALGLALNVPSSSHDTLCT---SCTGFPLSTRVPG 178
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 172 ACAPGTFSDTTSSTDVCRPHRICSLA---IPGNASTDAVCAPESPTLSAIPRTLYVSG 227
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 179 AEECEAAVIDFVAQDISIKRLQQLQALEAPBGWPTP-----RAGRALQLKRRRLT 233
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 228 PEPTRSQPLD---QEGPQSPQPSILTSL-----GSTPIIEOSTKGISLPIGLIVGT 277
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 234 ELGAQDGLLVRLQLA---RVAMPGLERSVRERFLP 269
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 278 SL-----GLMLGLVNCFTLVQRKKKPSCLQRDAKVPHPV 312
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
0912M6 PRELIMINARY; PRT; 433 AA.
AC 0912M6;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Tumor necrosis factor receptor type II (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY;
RA Osburg B., Belser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
   capillary endothelial cells and participate in TNF-alpha transport
   through the blood-brain barrier.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF000208; TNFR_c6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KM Receptor.
FT NON_TER 1 1
FT VARIANT 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 21.0%; Score 313.5; DB 11; Length 433;
Best Local Similarity 35.1%; Pred. No. 1.6e-19;
Matches 59; Conservative 29; Mismatches 67; Indels 13; Gaps 4;

QY 17 RLVAOCPPGTGVORPCRRDSPTTCGCPPRHYTQFWNYLERGYCNVLGGEREERARAC 76
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 32 QMCCAKCPGQYVAKHFNCKNTSDTVACADCEASMTYQVWNLHTCLSCSSCSTDQVETHTNC 91
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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QY 77 HATHNRACRTGFFA-----HAG---FCLHASCPGAGVIAPGTPSONTCQCPGPTF 129
DB 92 TKQNRVCANADSYCALUHGNCRCQMKLSCGPGFGVARSRISNGNVICSACAPGTF 151
QY 130 SASSSSQCPHRNCTALGLALNVPGSSGSHDTLCTCTGTFPLSTRVP 177
DB 152 SDTSSDVCPRHRICSILA-----IPGNASTDAVCASES--PTPSAVP 193

RESULT 7
Q98SM6 PRELIMINARY; PRT; 651 AA.
AC Q98SM6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Death receptor 6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.2; -.
DR HSP; P19438; INCF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR003975; Shal_channel.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01497; SHALCHANNEL.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;

Query Match 19.2%; Score 287; DB 13; Length 651;
Best Local Similarity 33.5%; Pred. No. 5.2e-17;
Matches 54; Conservative 27; Mismatches 80; Indels 0; Gaps 0;

QY 11 DAETGERLVCAQCPGTFVQRPCCRRDSPTTCGCPPRHYTQFWNYLRCRYCNVLCGERE 70
DB 43 DRATNQELICDKCPAGTVSVKHCTKSTLRCEPCPDGDTFTKHENGIERCHPKPCBLPM 102
QY 71 EEARACHATHNRACRTGFFAHAGFCLERHASCPPGAGVIAPGTPSQTCQCPGPTFS 130
DB 103 IEKTHCTALTDRECTLSGTFQINDTCVPTVCPVGWGRKKGKTETEDVRCKPCLRTFS 162
QY 131 ASSSSSQCPHRNCTALGLALNVPGSSGSHDTLCTCTGTF 171
DB 163 DVPSSVMKCTYTDTCFGKNMVMVVRPGTKESDNVCGSPASLP 203

RESULT 8
O57103 PRELIMINARY; PRT; 348 AA.
AC O57103;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB34367.1; -.
DR HSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 18.4%; Score 275; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 3e-16;
Matches 59; Conservative 29; Mismatches 82; Indels 8; Gaps 3;

QY 10 RDAETGER-LVCAQCPGTFVQRPCCRRDSPTTCGCPPRHYTQFWNYLRCRYCNVLCGE 68
DB 33 KDNEYRSRLCCLSCPPGTIVASRLCDSKNTQCTPCGSDTFTSHNNHLQACLSCNGRCD 92

Query Match 18.4%; Score 275; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 3e-16;
Matches 59; Conservative 29; Mismatches 82; Indels 8; Gaps 3;

QY 10 RDAETGER-LVCAQCPGTFVQRPCCRRDSPTTCGCPPRHYTQFWNYLRCRYCNVLCGE 68
DB 33 KDNEYRSRLCCLSCPPGTIVASRLCDSKNTQCTPCGSDTFTSHNNHLQACLSCNGRCD 92
QY 69 REEARACHATHNRACRTGTF-----AHAGFCLERHASCPPGAGVIAPGTPSQTCQ 122
DB 93 NOVETRSCTNTHNRICECSPGYCLLKSGSGCRTCSKTKGIGYGV-SGYTSTGDVICS 151
QY 123 PCPPGTFSSASSSEOCOPHRNCTALGLALNVPGSSGSHDTLCTCTGTFPLSTRVP 180
DB 152 PCGPGTSHVSTDRKCEPVTSTNFYIDVEINLYPNVDFSCRTTTTGLSEISISTSE 209

RESULT 9
O57108 PRELIMINARY; PRT; 348 AA.
AC O57108;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB34367.1; -.
DR HSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 18.4%; Score 275; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 3e-16;
Matches 59; Conservative 29; Mismatches 82; Indels 8; Gaps 3;

QY 10 RDAETGER-LVCAQCPGTFVQRPCCRRDSPTTCGCPPRHYTQFWNYLRCRYCNVLCGE 68
DB 33 KDNEYRSRLCCLSCPPGTIVASRLCDSKNTQCTPCGSDTFTSHNNHLQACLSCNGRCD 92
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QY 69 REEFARACHATHNACRCRTGFF-----AHAGFCLHASCPPGAGVIAPGTPSONTQO 122  
 DB 93 NOVETRSCTNTHNRICGSPGYCLIKSGSCRTICSTKCGIGYV-SGYSTGVDICS 151  
 QY 123 PCPPTGFSASSSSSEOCOPHRNCALGALNVPGSSSHDPLCTSCGFPPLSTRVPGA 180  
 DB 152 PCGPGTSHVSTDKCEPVTSTNTFNIVDVEINLPVNDISCTRTTTTGLSEISISTSE 209

## RESULT 10

057277 PRELIMINARY; PRT; 348 AA.  
 ID 057277;  
 AC 057277;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Tumor necrosis factor receptor II homolog (J2R) (J2L).  
 GN CRMB OR J2R OR J2L.  
 OS Monkeypox virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NCBI\_TaxID=10244;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZAIRE-1996 / 96-17, AND ZAIRE-1996 / 96-16;  
 RX Loparev V.N., Parsons J.M., Esposito J.J.;  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZAIRE-96-I-16;  
 RX MEDLINE=21592287; PubMed=11734207;  
 RA Shchelnikov S.N., Totmenin A.V., Babkin I.V., Safonov P.F.,  
 RA Ryzankina O.I., Petrov N.A., Gutorov V.V., Uvarova E.A.,  
 RA Mikheev M.V., Sisler J.R., Esposito J.J., Jahrling P.B., Moss B.,  
 RA Sandakhchiev L.S.;  
 RT "Human monkeypox and smallpox viruses: genomic comparison.";  
 RL FEBS Lett. 509:66-70(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZAIRE-96-I-16;  
 RA Shchelnikov S.N., Totmenin A.V., Safonov P.F., Gutorov V.V.,  
 RA Ryzankina O.I., Petrov N.A., Babkin I.V., Uvarova E.A.,  
 RA Esposito J.J., Moss B., Sisler J.R., Jahrling P.B., Sandakhchiev L.S.;  
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U87841; AAB94358.1; -;  
 DR EMBL; AF380138; AAL40648.1; -;  
 DR EMBL; AF380138; AAL40640.1; -;  
 DR HSSP; O14763; 1DOG.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00208; TNFR\_2.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

Query Match 18.4%; Score 275; DB 12; Length 348;

Best Local Similarity 33.1%; Pred. No. 3e-16; Mismatches 82; Indels 8; Gaps 3;

QY 10 RDAETGER-LVCAQCPPTGVQPCRRDSEPTTCGPPRRHYTGFMYLERCRCYNVLCGE 68  
 DB 33 KDNVEYRNRNLCCLSPGTYASRLCDKNTQCTPCGSDPTFTSHNNHLQACLSNGRCDS 92  
 QY 69 REEFARACHATHNACRCRTGFF-----AHAGFCLHASCPPGAGVIAPGTPSONTQO 122  
 DB 93 NOVETRSCTNTHNRICGSPGYCLIKSGSCRTICSTKCGIGYV-SGYSTGVDICS 151  
 QY 123 PCPPTGFSASSSSSEOCOPHRNCALGALNVPGSSSHDPLCTSCGFPPLSTRVPGA 180  
 DB 152 PCGPGTSHVSTDKCEPVTSTNTFNIVDVEINLPVNDISCTRTTTTGLSEISISTSE 209

RESULT 11  
 057100 PRELIMINARY; PRT; 349 AA.  
 ID 057100;  
 AC 057100;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Tumor necrosis factor receptor II homolog.  
 GN CRMB.  
 OS Monkeypox virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NCBI\_TaxID=10244;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIGERIA-1971;  
 RA Loparev V.N., Parsons J.M., Esposito J.J.;  
 RT "DNA sequence analysis as a criterion for allocation of the  
 RT orthopoxviruses to a particular species.";  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U87844; AAB94361.1; -;  
 DR HSSP; O14763; 1DOG.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00208; TNFR\_2.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KM Receptor.  
 SQ SEQUENCE 349 AA; 38239 MW; DFEC280D478F2422 CRC64;

Query Match 18.1%; Score 270.5; DB 12; Length 349;  
 Best Local Similarity 32.6%; Pred. No. 7.4e-16;  
 Mismatches 59; Conservative 29; Mismatches 80; Indels 13; Gaps 5;

QY 10 RDAETGER-LVCAQCPPTGVQPCRRDSEPTTCGPPRRHYTGFMYLERCRCYNVLCGE 68  
 DB 33 KDNVEYRNRNLCCLSPGTYASRLCDKNTQCTPCGSDPTFTSHNNHLQACLSNGRCDS 92  
 QY 69 REEFARACHATHNACRCRTGFF-----AHAGFCLHASCPPGAGVIAPGTPSONTQO 122  
 DB 93 NOVETRSCTNTHNRICGSPGYCLIKSGSCRTICSTKCGIGYV-SGYSTGVDICS 151  
 QY 123 PCPPTGFSASSSSSEOCOP---HRNCTALGALNVPGSSSHDPLCTSCGFPPLSTRVPGA 179  
 DB 152 PCGPGTSHVSTDKCEPVTSTNTFNIVDVEINL--YVNDISCTRTTTTGLSEISISTS 209  
 QY 180 E 180  
 DB 210 E 210  
 RESULT 12  
 057101 PRELIMINARY; PRT; 349 AA.  
 ID 057101;  
 AC 057101;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Tumor necrosis factor receptor II homolog.  
 GN CRMB.  
 OS Monkeypox virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 NCBI\_TaxID=10244;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ZAIRE-1977;  
 RA Loparev V.N., Parsons J.M., Esposito J.J.;  
 RT "DNA sequence analysis as a criterion for allocation of the  
 RT orthopoxviruses to a particular species.";  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U87845; AAB94362.1; -;  
 DR HSSP; O14763; 1DOG.

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DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38311 MW; 02F65B00CFB858BE CRC64;

Query Match      18.0%; Score 268.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 1.1e-15;
Matches 59; Conservative 29; Mismatches 80; Indels 13; Gaps

QY 10 RDAETGER-LVCAQCPCPTFFVORPCRERDSPTTCGCPPRHYTFQFWNYLERCRYCNVLGE 68
   :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 KDNEYRSNLCCLSCPPGTYSRLCDSKNTTQCTPGSDTFTSHNNHLQAACLSNCGRCD 92

QY 69 REEARACHATHNRACRKTGF-----AHAGFCLEHASCPPGAGVIAPGTPSONTQQ 122
   :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93 NQVEFRSCNTHNRICECSPGYYCLKSGSGGRTCI SKTKCGIGYG-VGYTSTGDVICS 151

QY 123 PCPPTGFSASSSSSQOCP---HNRCTALGLALNVPGSSSHDTLCTCTCGFPPLSTRVPGA 179
   :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 152 PCGCTGYSHTVSDDCKEPPVTSTNFNIYDVEINL--YPVNDSCTRTTTGLESISITS 209

QY 180 E 180
   |
Db 210 E 210

RESULT 13
ID O57102 PRELIMINARY; PRT; 349 AA.
AC A
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid:10244;
[1]
RN R
RP R
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87846; AAB94363.1; -.
DR HSP; O14763; IDOG.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 349 AA; 38308 MW; CBD2C949F994C59C CRC64;

Query Match      18.0%; Score 268.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 1.1e-15;
Matches 59; Conservative 29; Mismatches 80; Indels 13; Gaps

QY 10 RDAETGER-LVCAQCPCPTFFVORPCRERDSPTTCGCPPRHYTFQFWNYLERCRYCNVLGE 68
   :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 KDNEYRSNLCCLSCPPGTYSRLCDSKNTTQCTPGSDTFTSHNNHLQAACLSNCGRCD 92

QY 69 REEARACHATHNRACRKTGF-----AHAGFCLEHASCPPGAGVIAPGTPSONTQQ 122
   :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93 NQVEFRSCNTHNRICECSPGYYCLKSGSGGRTCI SKTKCGIGYG-VGYTSTGDVICS 151

QY 123 PCPPTGFSASSSSSQOCP---HNRCTALGLALNVPGSSSHDTLCTCTCGFPPLSTRVPGA 179
   :|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RP SEQUENCE FROM N.A.  
RC STRAIN=SIERRA LEONE-1970;  
RA Loparev V.N., Parsons J.M., Espósito J.J.;  
RT "DNA sequence analysis as a criterion for allocation of the  
orthopoxviruses to a particular species."  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U87843; AAB94360.1; -.  
DR HSSP; O14763; 1D0G.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00209; TNFR\_2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor.  
SQ SEQUENCE 349 AA; 38321 MW; FE449028C933F57 CRC64;

Query Match 17.9%; Score 267.5; DB 12; Length 349;  
Best Local Similarity 32.6%; Pred. No. 1,4e-15;  
Matches 59; Conservative 28; Mismatches 81; Indels 13; Gaps 5;

QY 10 RDAETGER-LVCAQCPGTFVORPCRRDSPPTCGPCPPRHYYTQPMNYLERCRYGNVLCGE 68  
Db 33 KDNFYRSRNLCCLSCPGTYSRLCDSKINTQCTPCGSDTFTSHNHLOACLSCNGRCD 92  
QY 69 REEFARACHATNNRACRCRTGFFA-----HAGFCLHASCPCGAGVIAPGTPSONTQCQ 122  
Db 93 NOVETRSCTNTHNRICGSPGYCLKGALGCRFCISKCKGIGYV-SGYTSTGDVICS 151  
QY 123 PCPPGTSSASSSSSEQCP--HNC TALGLALNVPSSSHDTLCTSGTFPLSTRVPGA 179  
Db 152 PCGGTYSHVSTDKCEPVVTSNTFNYIDIVEINL--YVNDTSCTRTTTTGLSESISTS 209  
QY 180 E 180  
Db 210 E 210

Search completed: January 6, 2003, 11:20:08  
Job time : 75 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Comphen Ltd.

# OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 6, 2003, 11:21:05 ; Search time 1970 Seconds  
(without alignments)  
2227.907 Million cell updates/sec

Title: US-09-936-024-1  
Perfect score: 1491  
Sequence: 1 VAETPTYPWRDAETGERLVC.....RVAMPGLERSVREPLFVH 271

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n model -DEV=xlh  
-O=/cgn2.1/USPTC/spool/US0993602/runat\_06012003\_111607\_12141/app\_query.fasta\_1.455  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -STRAT=1 -END=1 -MATRIX=bloms62 -TRANS=human40.coi -LIST=45  
-DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US0993602@cgn2.1 1.1349 @runat\_06012003\_111607\_12141 -NCPu=6 -ICPU=3  
-NO\_XLPHY -NO\_MMAR -LARGEOUTERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.\*  
1: em\_estba.\*  
2: em\_estchum.\*  
3: em\_estcin.\*  
4: em\_estcnu.\*  
5: em\_estcov.\*  
6: em\_estcpl.\*  
7: em\_estcro.\*  
8: em\_estc.\*  
9: gb\_estc1.\*  
10: gb\_estc2.\*  
11: gb\_estc3.\*  
12: gb\_estc4.\*  
13: gb\_estc5.\*  
14: gb\_estc.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: gb\_ggs.\*  
18: em\_ggs\_hum.\*  
19: em\_ggs\_inv.\*  
20: em\_ggs\_pln.\*  
21: em\_ggs\_vit.\*  
22: em\_ggs\_fun.\*  
23: em\_ggs\_mam.\*  
24: em\_ggs\_mus.\*  
25: em\_ggs\_other.\*  
26: em\_ggs\_pro.\*  
27: em\_ggs\_tod.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	1183	79.3	1118	13	BI821789
2	1147	76.9	863	12	BO687526
3	1069	71.7	617	12	BE878908
4	1064	71.4	572	14	BM767535
5	1060	71.1	1037	12	BG679499
6	1055	70.8	1203	13	BM480312
7	1034.5	69.4	728	14	BM680786
8	1020	68.4	679	12	BE878006
9	941.5	63.1	874	12	BF339551
10	866	58.1	554	10	AW464298
11	865.5	58.0	692	10	AW483241
12	836	56.1	588	13	BI838357
13	813	54.5	600	10	AW262121
14	793	53.2	605	14	BM767088
15	793	53.2	605	14	BM767418
16	793	53.2	606	14	BM767446
17	788	52.9	568	14	BO019285
18	781	52.4	596	14	BM767064
19	781	52.4	616	14	BM743072
20	769	51.6	486	14	BM831338
21	769	51.6	588	14	BM756087
22	769	51.6	593	14	BM759026
23	725	48.6	551	12	BE879166
24	725	48.6	697	12	BE873766
25	679	45.5	1216	14	BO716334
26	676	45.3	384	14	BM738195
27	670	44.9	540	10	AW471440
28	653	43.8	514	10	AW662363
29	644	43.2	475	9	AI718743
30	633	42.5	524	14	BM833454
31	604	40.5	478	12	BF001490
32	586	39.3	500	14	BM833463
33	584	39.2	515	10	AW083914
34	580	38.9	448	10	AW014771
35	566	38.0	448	14	BM672727
36	546	36.6	445	9	AI857725
37	523	35.1	453	10	AW204999
38	508	34.1	436	9	AI290210
39	503	33.7	467	9	AA025673
40	495	33.2	430	9	AI561219
41	495	33.2	452	10	AW771720
42	489	32.8	295	10	AW801019
43	487.5	32.7	428	9	AA155701
44	469	31.5	417	10	AW006931
45	462	31.0	399	10	AW080544

## ALIGNMENTS

RESULT 1  
BI821789  
LOCUS 603035863F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5176910 5',  
DEFINITION mRNA sequence.  
ACCESSION BI821789  
VERSION BI821789.1 GI:15933339  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1118)  
NIH-MGC http://mgs.nci.nih.gov/.  
TITLES National Institutes of Health (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11440 row: n column: 15  
High quality sequence stop: 758.  
Location/Qualifiers

## FEATURES

source  
1. .1118  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5176910"  
/clone\_lib="NIH\_MGC\_115"  
/lab\_host="DH10B"  
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SpORF6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."

BASE COUNT 223 a 377 c 339 g 173 t  
ORIGIN

Alignment Scores:  
Pred. No.: 9,73e-90 Length: 1118  
Score: 1163.00 Matches: 231  
Percent Similarity: 98.30% Conservative: 0  
Best Local Similarity: 98.30% Mismatches: 3  
Query Match: 79.34% Indels: 4  
DB: 13 Gaps: 0

US-09-936-024-1 (1-271) x BI821789 (1-1118)

QY 38 ProThrThrCysGlyProCysProProArgHisThrThrGlnPheTProAsnTyrLeuGlu 57  
DB 3 CCCACGACGTGG-CGGTGTCCACCGCGCCACTACACGCGAGTTCTGGAACTACTCTGGAG 61  
QY 58 -ArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluAlaAlaCysHis 77  
DB 62 CGCGTGGCGGTACTGCAACGTCCTCTCGGGGAGCGGTGAGGAGGAGGACCGGGTTGCCA 121  
QY 77 sAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCy 97  
DB 122 CGCCACCACAAACCGTGCCTGCCGCTCGCACCGGCTTCTTCGCGCAGCGTGGTTCTG 181  
QY 97 sLeuGluHisAlaSerCysProProGlyAlaGlyValleAlaProGlyThrProSerGl 117  
DB 182 CTTTGAGCAGCAGTCATGTCACCTGTGTGCGGGGTGAT-GCCCCGGGACCCGCCACCA 240  
QY 117 nAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSerSerGl 137  
DB 241 GAACACGAGTGCAGCGGTGCCCCCAGGACCTTCTCAGCCAGAGCTCCAGCTCAGA 300  
QY 137 uGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySe 157  
DB 301 GCAGTGCAGCCCCACCGCAACTGCACGGCCCTGGGCTCTCAATGTGCCAGGCTC 360  
QY 157 rSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValPr 177  
DB 361 TTCTCCCATGACACCTGTGCACCACTGCACCTGGTTCCTCCCTCAGCACCGGTA-CC 419  
QY 177 oGlyAlaGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIl 197  
DB 420 AGGAGCTGAGGAGTGTGAGCGTGCCTCATCGACTTTTGTGGCTTTCAGGACATCTCAT 479

QY 197 eLysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTroGlyProThrPr 217  
DB 480 CAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCGGGCTGGGGTCCGACAC 539  
QY 217 oArgAlaGlyArgAlaAlaLeuGlnLeuLysLeuArgArgArgLeuThrGluLeuLeuGl 237  
DB 540 AAGGGCGGGCGCGCGCTTGAGCTGAGCTGCGTGGCGGCTCAGGAGGCTCTCTGGG 599  
QY 237 YAlaGlnAspGlyAlaLeuLeuValArgLeuGlnAlaLeuArgValAlaArgMetPr 257  
DB 600 GGGCGAGGACGGGGCGCTGCTGCTGGCTGCTGCAGGCGCTGCGCTGGCCAGGATGCC 659  
QY 257 oGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271  
DB 660 CGGCTGGAGCGGAGCGTCCGTGAGCGCTTCCTCCCTGTGCAC 702  
RESULT 2  
LOCUS BQ687526 863 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8345883 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6250691  
5', mRNA sequence.  
ACCESSION BQ687526  
VERSION BQ687526.1 GI:21812842  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1. (bases 1 to 863)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2394 row: c column: 12  
High quality sequence stop: 599.  
Location/Qualifiers  
source  
1. .863  
/organism="Homo sapiens"  
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/clone="IMAGE:6250691"  
/clone\_lib="NIH\_MGC\_110"  
/tissue\_type="ductal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 133 a 312 c 276 g 141 t  
ORIGIN

## Alignment Scores:

Pred. No.: 7,56e-87 Length: 863  
Score: 1147.00 Matches: 220  
Percent Similarity: 94.87% Conservative: 2  
Best Local Similarity: 94.02% Mismatches: 5  
Query Match: 76.93% Indels: 7  
DB: 14 Gaps: 2

US-09-936-024-1 (1-271) x BQ687526 (1-863)



```

Qy 1 ValAlaGluThrProThyTyProTTPaRgAspAlaGluThrGlyGluArgLeuValCys 20
Db 149 GTGGGAGAAACACCCACCTACCTGCGGAGACGACAGACAGGGGAGCGGTGTGT 208
Qy 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 209 GCCAGTGGCCCCCAGGACCTTTGTGACAGCGCGCGCGCCGACAGACCCCGACAGC 268
Qy 41 CysGlyProCysProProAArgHisTyThrGlnPheThrAsnTyLeuGluArgCysArg 60
Db 269 TGTGGCCCCGTGTCCACCGCCGACCTACACGAGTTCTGGAACTCTCGAGCGCTGCCCG 328
Qy 61 TyTCysAsnValLeuCysGlyGluArgGlnGluValaArgAlaCysHisAlaThrHis 80
Db 329 TACTGCAACGTCCTCTCGGGGAGCGTGAAGAGAGGAGGAGCGGTTCGACAGCCAC 388
Qy 81 AsnArgAlaCysArgCysArgThyGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 389 AACGCGCCCTGCCCTCCGACCGGACCGGCTTCTTCGCGACAGCTGTGTTCTGTGAGAC 448
Qy 101 AlAserCysProProGlyValaGlyValaIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 449 GCATCGTGTCACTGTGTGCGGCGGTGATGCCCCGGGACACCCCGACGACAGACGAG 508
Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGlnCysGln 140
Db 509 TGCACGCGTGGCCCCCAGGACCTTCTCAGCCGACGAGTTCCAGCTCAGAGCACTGGCAG 568
Qy 141 ProHisArgAsnCysThr-AlaLeuGlyLeu-AlaLeuAsnValProGlySerSerSerH 160
Db 569 CCCCACCGCAACTGCACGAGCGCTGGGCGCTGCACATGTCGACGAGCTTCTTCC 628
Qy 160 HisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGly-Ala 179
Db 629 ATGACACGCTGTGACACGAGCTGACGTGCTTCCCTCAGACAGGAGTACAGAGAGCT 688
Qy 180 GlnGlu-CysGlnArgAlaValaIleAsp-PheValAlaPheGlnAspIleSerIleCysA 199
Db 689 GAGGAAGTGTGAGGTGCGGTGATGCTTGTGTGCTTCCAGACATCTCCATCAAGA 748
Qy 199 rgleuGlnArgLeuGlnAlaLeuGlnAlaProGlyGlyTyrGly--ProThrProA 218
Db 749 AGCTGCAGCGGCTGCTCAGGCGCTCGAGGCGCCGGAAGGGGTGGGGTCCGAACCA 808
Qy 218 rgaIaGly---ArgAlaAlaLeuGlnLeuys 227
Db 809 GGGGCGGGCGCGCCCGGCGCTTGCACACTTGA 840

RESULT 3
BE878908 617 bp mRNA linear EST 20-OCT-2000
DEFINITION 601492609F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894794 5',
ACCESSION BE878908
VERSION BE878908.1 GI:10327684
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 617)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgs@bbs-rcmail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

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    /note="Organ: lung; Vector: pCMV-SORT6; Site_1: NotI;
    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.1 kb. Library constructed by Life
    Technologies."
BASE COUNT 91 a 224 c 203 g 99 t
ORIGIN
Alignment Scores:
Pred. No.: 1,85e-80 Length: 617
Score: 1069.00 Matches: 202
Percent Similarity: 98.54% Conservative: 0
Best Local Similarity: 98.54% Mismatches: 3
Query Match: 71.70% Indels: 1
DB: 12 Gaps: 0

US-09-936-024-1 (1-271) x BE878908 (1-617)
Qy 53 TTPAsnTyLeuGlnArgCysArgTyTCysAsnValLeuCysGlyGluArgGlnGlu 72
Db 4 TGGAACTACCTGAGCGCTGCTCCCTACTGCAACGTCCTCTGCGGAGCGTGAAGAGAG 63
Qy 73 AlArGAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThyGlyPhePheAla 92
Db 64 GCAAGGCTTGCACGCGCACCAACCGTCTGCGCGTCCGCGACCGGCTTCTTCCG 123
Qy 93 HisAlaGlyPheCysLeuGlnHisAlaSerCysProProGlyValaGlyValaIleAlaPro 112
Db 124 CACGCTGTTTGTGCTTGGAGACGACATCGTGTCCACTGCTGCGGCGCGGATGATGCCCG 183
Qy 113 GlyThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSer 132
Db 184 GGCACCCCGCAGAACAGACAGTGCACCGCTGCCCCCAGGACACTTCTCAGCGAGC 243
Qy 133 SerSerSerSerGlnGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeu 152
Db 244 AGCTCCAGCTCAGAGAGTGCACCGCCCGCACTGCAAGGCTTGGGCTTGGCCCTC 303
Qy 153 AsnValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeu 172
Db 304 AATGTGCCAGGCTTCTCTCCATGACACCTGTGACACAGCTGCACTGGCTTCCCTC 363
Qy 173 SerThrArgValProGlyAlaGlnGluCysGlnArgAlaValaIleAspPheValAlaPhe 192
Db 364 AGCACCGAGGTACAGAGAGTGAAGAGTGAAGGTCCTGCTCATGCACTTGTGTGCTTTC 423
Qy 193 GlnAspIleSerIleCysArgLeuGlnArgLeuGlnAlaLeuGlnAlaProGlyGly 212
Db 424 CAGGACATCTCCATCAAGAGGCTGACGCGCTGTGAGGCTTCCAGAGCCCGGAGGAG 483
Qy 213 TTPGlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuysLeuArgArgArgLeu 232
Db 484 TGGGTGTCGACACCAAGGGGGGCGCGCGGCTTTCAGAGTGAAGCTGCGTGGCGGCTC 543
Qy 233 ThrGlnLeuGlnGlyAlaGlnAspGlyAlaLeuLeuValaArgLeuGlnAlaLeuArg 252
Db 544 ACGAGGCTCTCTGGGGGCGAGACGGGGCGCTGTGTGTGGTGTG-CTGACAGCGCTTGGC 602
Qy 253 ValAlaArgMetPro 257
Db 603 GTGGCAGAGATGCCG 617

RESULT 4
BM767535

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LOCUS  
DEFINITION K-EST0050015 S1SNU5s2 Homo sapiens CDNA clone S1SNU5s2-3-E03 5', linear mRNA 572 bp EST 04-MAR-2002

ACCESSION  
VERSION BM767535  
KEYWORDS  
SOURCE EST.  
ORGANISM human, GI:19097150

REFERENCE  
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE  
JOURNAL 21c Frontier Korean EST Project 2001  
COMMENT Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 3 row: E column: 03  
High quality sequence stop: 572.  
Location/Qualifiers

FEATURES  
source  
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/sex="F"  
/tissue\_type="Ascites"  
/cell\_type="Lymphoblast-like"  
/cell\_line="SNU-5"  
/lab\_host="Top10p"  
/note="Organ: Stomach; Vector: pcNS; Site\_1: EcoRI; Site\_2: NotI; The poly (A) RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with di-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10p by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10p with electroporation method."

BASE COUNT 90 a 213 c 174 g 95 t  
ORIGIN

Alignment Scores:  
Pred. No.: 4,43e-80 Length: 572  
Score: 1064.00 Matches: 190  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 71.36% Indels: 0  
DB: 14 Gaps: 0  
US-09-936-024-1 (1-271) x BM767535 (1-572)

QY 40 ThrCysGlyProCysProArgHisTyrThrGlnPheTyrAsnTyrLeuGluAlaGlyCys 59  
|||||  
Db 2 ACGTGTGGCCCGGTGTCACCGGCCACTACACGAGTTCTGGAACTACTCTGGAGCGCTGC 61  
|||||  
QY 60 ArgTyrCysAsnValLeuGluGlyGluArgGluGluAlaAargAlaCysHisAlaThr 79  
|||||  
Db 62 CGCTACTGCAACGTCCTCTCGGGGAGCGTGAGGAGGAGGACGGGCTTGGCCAGCCACC 121  
|||||  
QY 80 HisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGlu 99  
|||||  
Db 122 CACAACCGCGCTGCGGCTGCCGACCGGCTTCTTCGCGACGCTGGTTCTCTTTGGAG 181  
|||||  
QY 100 HisAlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThr 119  
|||||  
Db 182 CAGCGATCGTGTCACCTGTCGGCGGTGATTCGCCGGGACCCCGGACAGACACG 241  
|||||  
QY 120 GlnCysGlnProCysProGlyThrPheSerAlaSerSerSerSerSerGluGlnCys 139  
|||||  
Db 242 CAGTGCAGCGCGTCCCGCCAGGCACCTTCTCAGCCAGCAGATTCCAGCTCAGAGCAGTGC 301  
|||||  
QY 140 GlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSer 159  
|||||  
Db 302 CAGCCCCACCGCAACTGCACGGCCCTGGGCGCTGCGCCCTCAATGTGCAGGCTCTTCCTCC 361  
|||||  
QY 160 HisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAla 179  
|||||  
Db 362 CATGACACGCTGTGCACAGCTGCATGCTGCTTCCCTTCCAGCAGGATACGAGAGCT 421  
|||||  
QY 180 GluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleLysArg 199  
|||||  
Db 422 GAGGAGTGTGAGCGTCCGCTCATCGACTTTGTGGCTTTCCAGGACATCTCCATCAAGAGG 481  
|||||  
QY 200 LeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAla 219  
|||||  
Db 482 CTGCAGCGCTGTGTGAGGCGCTTCGAGGCGCTTCGAGGCGGCTGGGGTCCGACACCAAGGGCG 541  
|||||  
QY 220 GlyArgAlaAlaLeuGlnLeuLysLeuArg 229  
|||||  
Db 542 GGCCGCGCGGCTTGCAGCTGAAGCTGCGT 571  
|||||

RESULT 5  
BG679499  
LOCUS  
DEFINITION BG679499 1037 bp mRNA linear EST 01-MAY-2001  
602527314F1 NCI\_CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4752507 5', mRNA sequence.

ACCESSION BG679499  
VERSION BG679499.1 GI:13910896  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1037)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-romail.nih.gov](mailto:cgapbs-romail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10610 row: k column: 04  
High quality sequence stop: 762.  
Location/Qualifiers

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source
1. 1037
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:4752507"
/clone_1ib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: PCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT      153 a      364 c      337 g      183 t
ORIGIN

Alignment Scores:
Pred. No.:      2,06e-79      Length:      1037
Score:          1060.00      Matches:      216
Percent Similarity: 86.77%      Conservative: 7
Best Local Similarity: 84.05%      Mismatches: 24
Query Match:      71.09%      Indels:      12
DB:              12      Gaps:      3

US-09-936-024-1 (1-271) x BG679499 (1-1037)

QY 1 ValAlAGluThrProThyTyProTPrAgsPAlAGluThrglyuaTgLeuValCys 20
Db 195 GTGGCAGAAACACCACTTACCTGCGGAGACGACAGACAGGAGGCGGCTGTGTC 254

QY 21 AlAGlncysProProglYThrPheValGlnArGProCysArGArGArSerpProThr 40
Db 255 GCCCAGTGCCTCCCGAGGACCTTGTGACGCGGCGCGCCGAGACACCCACACG 314

QY 41 CysGlyProCysProProArGhIstYrThGlnPheTrpAsnTyrluGluArgCysArg 60
Db 315 TGTGGCCCGGTCCACCGCCCTACACGAGTTCTGGAATCTACGAGCCCTGCGCG 374

QY 61 TyrcysAsnValleucysglyuaTgGlnGluAlaArGAlaCysHIsAlaThrHis 80
Db 375 TACTGCAAGCTCTCTGCGGAGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434

QY 81 AsnArGAlaCysArGArGThrglyPhePheAlaHIsAlaGlyPheCysLeuGluHis 100
Db 435 AACCGTGCCTCCCGAGGACCTTGTGACGCGGCGCGCCGCTGTTCTGTGAGAC 493

QY 101 AlaSerCysProProglYAlAGlValIleAlaProglYThrProSerGlnAsnThrGln 120
Db 494 GCATCGGTCCACCTGATGCGGCGGTGATGCGCGGAGAGAGAGAGAGAGAGAGAG 553

QY 121 CysGlnProCysProProglYThrPheSerAlaSerSerSerSerSerSerGlnCysGln 140
Db 554 TGCACAGCGGTGCGCCCGAGGACCTTCTCAGCCAGAGCTCCAGCTCAGAGAGTGCAG 613

QY 141 ProHIsArGAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProglYSerSerSerHis 160
Db 614 CCCACCGCAGAACTGCGG-GCCCTGGGCTGCGCTCAATGTGCAGAGCTCTTCCTTCAT 672

QY 161 AspThrLeu-CysThrSerCysThr-GlyPheProLeuSerTrpArgValProglYAlaG 180
Db 673 GAAACCTGTGACACAGCTGACCTGTGCTCCCTCCACACAGAGAGAGAGAGAGAGAG 732

QY 180 lncGluCysGln-ArGAlaVal-IleAspPheValAlaPhe-----GlnAspIleSerI 197
Db 733 AGAGAGTGAAGAGTGCCTGCTTCATCTTGTGGGCTTCCAGGAGAAATCTTCATC 792

QY 197 eLySArg-LeuGlnArgLeuLeuGlnAla---LeuGlnAlaProglYlTyPylY-Pro 215
Db 793 AAGAAAGCTTGCAGAGGAGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 852

QY 216 ThrProArgAlaIyArGAlaAlaLeuGlnLeuLySLeuArgArgArgLeuThrGlnLeu 235
Db 853 ACACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 912

QY 236 LeuGlyAla---GlnAspGlyAlaLeuLeuValArgLeu 247

```

```

Db 913 TCCGGGAGGCGCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 951
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RESULT 6
BM480312
LOCUS      BM480312      1203 bp      mRNA      linear      EST 05-FEB-2002
DEFINITION AGENCOURT 6424187 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491790
5', mRNA sequence.
ACCESSION  BM480312
VERSION    BM480312.1  GI:18529354
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 1203)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-rmemail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNL at:
            http://image.llnl.gov
            Plate: LLAM12112 row: n column: 15
            High quality sequence start: 4
            High quality sequence stop: 560.
            Location/Qualifiers
                source          1..1203
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5491790"
                /clone_1ib="NIH_MGC_67"
                /tissue_type="retinoblastoma"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: eye; Vector: PCMV-SPORT6; Site: 1: NotI;
                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.75 kb. Library constructed by Life
                Technologies."
                DB:              13      Gaps:      5

BASE COUNT      202 a      452 c      311 g      238 t
ORIGIN

Alignment Scores:
Pred. No.:      6.58e-79      Length:      1203
Score:          1055.00      Matches:      205
Percent Similarity: 78.65%      Conservative: 5
Best Local Similarity: 76.78%      Mismatches: 23
Query Match:      70.76%      Indels:      35
DB:              13      Gaps:      5

US-09-936-024-1 (1-271) x BM480312 (1-1203)

QY 1 ValAlAGluThrProThyTyProTPrAgsPAlAGluThrglyuaTgLeuValCys 20
Db 193 GTGGCAGAAACACCACTTACCTGCGGAGACGACAGACAGGAGGAGGAGGAGGAGGAG 252

QY 21 AlAGlncysProProglYThrPheValGlnArGProCysArGArGArSerpProThr 40
Db 253 GCCCAGTGCCTCCCGAGGACCTTGTGACGCGGCGCGCTGCGGAGACAGCCACAGAG 312

QY 41 CysGlyProCysProProArGhIstYrThGlnPheTrpAsnTyrluGluArgCysArg 60
Db 313 TGTGGCCCGGTCCACCGCCCTACACGAGTTCTGGAATCTACGAGGAGGAGGAGGAG 372

QY 61 TyrcysAsnValleucysglyuaTgGlnGluAlaArGAlaCysHIsAlaThrHis 80
Db 373 TACTGCAAGCTCTCTGCGGAGCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432

QY 81 AsnArGAlaCysArGArGThrglyPhePheAlaHIsAlaGlyPheCysLeuGluHis 100

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```
Db 433 AACCGTGCCTGCCGTCACCGGCTTCTTCGCGACGCTGTTCTGCTGGAGCAC 492
Qy 101 AlaSerCysProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 493 GCATCGTGTCCACCTGTTGCGCGGCTGATTGCCCGGGACCCCGACGAGCACGAG 552
Qy 121 CysGlnProCysProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
Db 553 TGCCAGCGGTGCCCGCCAGGACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAG 612
Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerHis 160
Db 613 CCCACCGCACTGCACGGCCCTGGGCTTCCCTCAATGTGCCAGGCTTCTCTCCAT 672
Qy 161 AspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArgValProGlyAla-G1 180
Db 673 GACACCTGTGCACCGCTGCACCTGGCTTCCCTCAGCAGGATACCAAGAGCTGA 732
Qy 180 uGluCysGluArgAlaValIleAspPheVal---AlaPheGln---AspIleSerIleLy 198
Db 733 GGAGTGTGAGCGTGCCTCCATCCACTTTGTGGGCTTTTCCAGGACCTCTCTCTCAA 792
Qy 198 sArgLeuGlnArgLeuLeu---GlnAlaLeuGluAlaPro----- 210
Db 793 AAGTTGTGAGCGGCTTCTGTCAGGCGCCCTCCAAAGGCCCGGTAAAGCTTGGGTGCC 852
Qy 211 -----GluGlyTrpGlyProThrProArg----- 218
Db 853 AACACCTAGGCGCGGACCGGGAGTACCCCTAACCTCATACACTTACCACCCCG 912
Qy 219 -----AlaGlyArgAlaAlaLeuGlnLeuLy 227
Db 913 AATCACACCCACTCTTTTGGCGCACCAATCCTCTGCGAGTTTCTGCTTTCAGCGCCC 972
Qy 227 sLeuArgArgLeuThr 233
Db 973 TCTCTC-CGTGCGCTTACA 990

RESULT 7
BM680786/c 728 bp mRNA linear EST 27-FEB-2002
LOCUS UI-E-E01-ajc-j-12-0-UI.s1 UI-E-E01 Homo sapiens cDNA clone
DEFINITION UI-E-E01-ajc-j-12-0-UI 3', mRNA sequence.
ACCESSION BM680786
VERSION BM680786.1 GI:18990682
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 728)
AUTHORS Ronaldo M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=Yes. Location/Qualifiers
```

## source

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1. 728
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-E01-ajc-j-12-0-UI"
/clone_lib="UI-E-E01"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-E01 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 8:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dt)18 tail. The sequence tag for this library is
CCGATATACC. This library was created for the program, Gene
Discovery in the Visual System, supported by National Eye
Institute (NEI).
TAG_LIB=UI-E-E01
TAG_TISSUE=human fetal eye
TAG_SEQ=CCGATATACC"
BASE COUNT 133 a 218 c 248 g 129 t
ORIGIN
```

## Alignment Scores:

```
Pred. No.: 1.85e-77 Length: 728
Score: 1034.50 Matches: 196
Percent Similarity: 98.99% Conservative: 0
Best Local Similarity: 98.99% Mismatches: 1
Query Match: 69.38% Indels: 1
DB: 14 Gaps: 1
```

US-09-936-024-1 (1-271) x BM680786 (1-728)

```
Qy 75 AlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPheAlaHisAla 94
Db 704 GCTTGCAGCAGCCACCAACCGTGCCTGCCGCTGCCGACCGGCTTCTCGCGCAGCT 645
Qy 95 GlyPheCysLeuGluHisAlaSerCysProGlyAlaGlyValIleAlaProGlyThr 114
Db 644 GGTTCCTGCTTGGAGCACGCATCGTCCACCTGTGTCGGCGGTGATTGCCCGGGCACC 595
Qy 115 ProSerGlnAsnThrGlnCysGlnProCysProGlyThrPheSerAlaSerSer 134
Db 584 CCCAGCCAGAACACGAGTGCCAGCGCTGCCCGCCAGGACCTTCTCAGCAGCAGCTCC 525
Qy 135 SerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnVal 154
Db 524 AGCTCAGAGCAGTGCCAGCGCCACCCACCACTGCACCGGCTTGGGCTTGGCCCTCAATG 465
Qy 155 ProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThr 174
Db 464 CCAGGCTTCTCTCCCATGACACCTGTGCACCGAGCTGCACCTGGCTTCCCTCCAGCACC 405
Qy 175 ArgValPro---GlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGln 193
Db 404 AGGTATACCAGCAGGAGCTGAGGAGTGTGAGCGTCCCGCTCATGCATCTTGTGGCTTTCCAG 345
Qy 194 AspIleSerIleLeysArgLeuGlnArgLeuLeuGlnAlaLeuGluAlaProGluGlyTrp 213
Db 344 GACATCTCCATCAGAGGCTGCAGCGGCTGCTGCAGCGCTTCCAGCGCCCGCGAGGCTGG 295
Qy 214 GlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLeuArgArgArgLeuThr 233
Db 284 GGTCCGACACCAAGGGCGGCGCGGCTTGCAGCTGAAGCTGCGTGGCGGCTCACG 225
Qy 234 GluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuGlnAlaLeuArgVal 253
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Db 224 GAGCTCTGGGGCGAGAGCGGGGCGCTGCTGCTGCGAGGGCGCTG 165
Qy 254 AAlaArgMetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271
Db 164 GCCAGATGCCCCGGGCTGAGAGCGGAGCGCTCGTAGCGCTTCTCCCTGTGCAC 111

RESULT 8
LOCUS BE878006 679 bp mRNA linear EST 20-OCT-2000
DEFINITION 601489784F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891908 5',
ACCESSION BE878006
VERSION BE878006.1 GI:10326782
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 679)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9677 row: h column: 21
High quality sequence stop: 672.
Location/Qualifiers
source
1..679
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3891908"
/clone_lib="NIH_MGC_69"
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 Kb. Library constructed by Life
Technologies."
BASE COUNT 113 a 239 c 204 g 123 t
ORIGIN

Alignment Scores:
Pred. No.: 2,82e-76 Length: 679
Score: 1020.00 Matches: 195
Percent Similarity: 99.49% Conservative: 0
Best Local Similarity: 99.49% Mismatches: 1
Query Match: 68.41% Indels: 1
DB: 12 Gaps: 0

US-09-936-024-1 (1-271) x BE878006 (1-679)
Qy 76 CysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGly 95
Db 1 TCCACAGCCAC-CACAAACGTCGCTGCGCTGCGACCGGCTTTCGCGACGCTGGT 59
Qy 96 PheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGlyThrPro 115
Db 60 TTCCTGTTGGAGACCGCATCGTCCACCTGGCGCGGCGGTGATTGCCCGGCGACCCCC 119
Qy 116 SerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSerSerSer 135
Db 120 AGCCAGAACACGACAGTGCACGCGCTGCCCCCGACGACCTTTCACGCGACGACCTCAAG 179
Qy 136 SerGlnGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAlaPro 155

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Db 180 TCAGACAGTCCAGCCCAACCGCAACTGCACGCGCCCTGGGCGCTCAATGTGCCA 239
Qy 156 GlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeuSerThrArg 175
Db 240 GGCTCTTCTCCATATACACCTGTGCACCACTGACAGTGGCTTCCCTCCACACACAG 239
Qy 176 ValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAlaPheGlnAspIle 195
Db 300 GTACACAGAGCTGAGGAGGTGAGCGTGCCTGCATGCACCTTGTGGCTTTCACGACATC 359
Qy 196 SerIleValArgLeuGluInArgLeuLeuGlnAlaLeuGluAlaProGluGlyThrGlyPro 215
Db 360 TCCATCAAGAGCGTCGACGCGCTGCTGCAGCGCCCTCGAGCGCCCGAGGCGCTGGGCTCCG 419
Qy 216 ThrProArgAlaGlyArgAlaAlaLeuGlnLeuValysLeuArgArgPheLeuThrGluLeu 235
Db 420 ACACCAAGGGGCGGGCGCGCTTTCAGCTGAACTGCTGCGGGGCTCACGGAGCTC 479
Qy 236 LeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuLeuGlnAlaLeuArgValAlaArg 255
Db 480 CTGGGGGCGCACAGACGGGCGCTGCTGTCGCGGCTGCTGCAGGCGCTGGCGCGCCAGG 539
Qy 256 MetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271
Db 540 ATGCCCGGCGCTGAGCGGAGCGCTCCGTGAGCGCTTCTCCCTGTGTGCAC 587

RESULT 9
LOCUS BF339551 874 bp mRNA linear EST 22-NOV-2000
DEFINITION 602039016F1 NCI CGAP Brn64 Homo sapiens cDNA clone IMAGE:4186995
5', mRNA sequence.
ACCESSION BF339551
VERSION BF339551.1 GI:11286006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 874)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM9508 row: p column: 04
High quality sequence stop: 701.
Location/Qualifiers
source
1..874
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4186995"
/clone_lib="NCI CGAP Brn64"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 Kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
BASE COUNT 129 a 299 c 301 g 145 t
ORIGIN

Alignment Scores:
Pred. No.: 1.61e-69 Length: 874
Score: 941.50 Matches: 181
Percent Similarity: 82.14% Conservative: 3
Best Local Similarity: 80.80% Mismatches: 27

```

```

Query Match: 63.15% Indels: 14
DB: 12 Gaps: 2

US-09-936-024-1 (1-271) x BF339551 (1-874)

Qy 1 ValAlaGluThrProThrTyProTyrArgAspAlaGluThrGlyGluArgLeuValCys 20
Db 185 GTGCAGAAACACACCTACCTCCCTGCGGACGCAGACAGAGGGAGCGCTGGTGTGC 244

Qy 21 AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr 40
Db 245 GCCAGTGTCCCGCCAGGACCTTTGTGACGCGCGCTGCGCCGAGACAGCCCCACGACG 304

Qy 41 CysGlyProCysProProArgHisTyThrGlnPheTyrAsnTyLeuGluArgCysArg 60
Db 305 TGTGCCCGTGTCCACCGCGCCACTACACGAGTCTTGGAACTACCTGGAGCGGTGCCGC 364

Qy 61 TyrCysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHis 80
Db 365 TACTGCAACGTCTCTGCGGGAGCGTGAGGAGGACGCGGTTCGCCAGCCGCCACCCAC 424

Qy 81 AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis 100
Db 425 AACCGTGTCTCCCGCTGCCGACCGGCTTCTTCGCGACGCTGTGTTCTGCTGGAGCAC 484

Qy 101 AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln 120
Db 485 GCATCGTGTCCACCTGTGTGCCGCGGTGATTGCCCGGGCACCCCGACGACCAACACG 544

Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSerSerGluGlnCysGln 140
Db 545 TGCCAGCGTGTCCCGCCAGGCAACCTTCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGC 604

Qy 141 ProHisArgAsnCysThrAlaLeuGlyLeuAlaLeuAsnValProGlySerSerSerHis 160
Db 605 CCCACCG-AACTGCAGCGCTGGGCGCTGCCTCAATGTGCCAGGCTCTTCTCCCAT 663

Qy 161 AspThrLeuCys-ThrSerCysThrGlyPheProLeuSerThrArgValProGlyAlaGln 180
Db 664 GACACCTGTGGCACCAGCTCAGCTGTTCCCGC---TCAGCACAGGTCAGGAGTTGA 720

Qy 180 uGlu-CysGluArgAlaValIleAspPheValAlaPheGlnAspIleSerIleIysArgL 200
Db 721 TGAAGTGTAGCGTGGCTCTCTGAGTTTGTGGCTTTCAGGAGACTCTCCATCAAGAGGT 780

Qy 200 euGlnArgLeuGlnAlaLeuGluAlaProGluGlyTyrGlyProThrProArgAlaG 220
Db 781 GC-----GCGGTGTGGCGCTTAGGCCCGCGAGGTGG 810

Qy 220 lyArgAla 222
Db 811 GGTCCGCC 818

RESULT 10
AW464298 554 bp mRNA linear EST 24-FEB-2000
LOCUS BP230015A20G11 Soares normalized bovine placenta Bos taurus cDNA
DEFINITION clone BP230015A20G11 5', mRNA sequence.
ACCESSION AW464298
VERSION AW464298.1 GI:7034466
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bos.
1 (bases 1 to 554)
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
CONTACT Lewin, H. A.
COMMENT W. M. Keck Center for Comparative and Functional Genomics

```

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University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATAGGACTCACTATAGG
BACKWARD: ATTAACCCCTCACTAAAG
Insert Length: 554 Std Error: 0.00
Plate: BP230015A20 row: G column: 11
Seq primer: AGCGGATACAAATTTTCACACAGGA
High quality sequence stop: 554.
Location/Qualifiers
1..554
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP230015A20G11"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI;
Site 2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."
M.B. (1996), Genome Research 6(9): 791-806."
BASE COUNT 76 a 213 c 184 g 81 t
ORIGIN
Alignment Scores: 2.08e-63 Length: 554
Pred. No.: 866.00 Matches: 147
Score: 91.62% Conservative: 6
Percent Similarity: 88.02% Mismatches: 14
Best Local Similarity: 58.08% Indels: 0
Query Match: 10 Gaps: 0
DB: 0
US-09-936-024-1 (1-271) x AW464298 (1-554)
Qy 2 AlaGluThrProThrTyProTyrArgAspAlaGluThrGlyGluArgLeuValCysAla 21
Db 52 GCAGCGCGCCCATCTACCGCTGGAGGAGCGAGAGCGGGGAGTGGCTGGTGTGTGAC 111
Qy 22 GlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThrCys 41
Db 112 CAGTGCCTCCGGCACCTTTGTGACGCGGCTTGGCGCGGAACAGCCCCAGACGTGC 171
Qy 42 GlyProCysProProArgHisTyThrGlnPheTyrAsnTyLeuGluArgCysArgTyr 61
Db 172 GGTGCGTGGCCCGCGCCACTACACAAATTTGGAACTACCTGGAGCGCTGCCGTAC 231
Qy 62 CysAsnValLeuCysGlyGluArgGluGluAlaArgAlaCysHisAlaThrHisAsn 81
Db 232 TGCNACGTCTATCTGCGGGAGCGGAGGAGGCGCGCGCTGCGGGGCCACCCACAC 291
Qy 82 ArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHisAla 101
Db 292 CGGCGCTTCCGCTGCTCGGTCCGTTTCTTCAGCACGCCCGCTTCTGCTGGAGACGCG 351
Qy 102 SerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrCys 121
Db 352 TCCTGCGCGCGCGCGCGGTGGTGTCTCCCGGACACCCCGACCCAGCCAGACACAGTGC 411
Qy 122 GlnProCysProProGlyThrPheSerAlaSerSerSerSerSerSerGluGlnCysGlnPro 141
Db 412 CAGCGGTGCCCGCGGACCTTCTCCGCCAGCAGCTCGAGCTCGGAGCGGTGCCAGCCC 471

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QY 142 HisArgAsnCyThrAlaLeuGlyLeuAlaLeuAnValProGlySerSerHisAsp 161  
 DB 472 CACCGCAACGACAGCCCTGGCGCTGCGTCAATGTGCTGCCGCTTACACGAC 531  
 QY 162 ThrLeuCyThrSerCyThr 168  
 DB 532 GCCCTGTGCACCACTGCAGC 552

RESULT 11  
 AM083241/c 692 bp mRNA linear EST 14-OCT-1999  
 LOCUS NC07404.x1 NCI CGAP\_C021 Homo sapiens cDNA clone IMAGE:2583534 3'  
 DEFINITION similar to TR:095407 095407 DEC0Y RECEPTOR 3. ; contains 1.1.b1 MER22  
 repetitive element ; , mRNA sequence.

ACCESSION AM083241.1 GI:6038393  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 692)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life  
 Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The  
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
 Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 www.bio.liml.gov/bdyp/image/image.html  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 414.

FEATURES  
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 1.692  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:2583534"  
 /clone\_lib="NCI CGAP C021"  
 /tissue\_type="moderately differentiated adenocarcinoma"  
 /lab\_host="DH10B"  
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Normalized to Cot >500. Average insert size 1.04kb.  
 Normalized version of NCI\_CGAP\_C018. Library constructed  
 by Life Technologies."

BASE COUNT 136 a 205 c 235 g 115 t 1 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 3.05e-63 Length: 692  
 Score: 865.50 Matches: 177  
 Percent Similarity: 89.95% Conservative: 2  
 Best Local Similarity: 88.94% Mismatches: 18  
 Query Match: 58.05% Indels: 3  
 Gaps: 1

US-09-936-024-1 (1-271) x AM083241 (1-692)

QY 74 ArgAlaCyHisAlaThrHisAsnArgAlaCyArgCySarThrGlyPhePheAlaHis 93  
 DB 689 CGGTCCCGACGCTTCACGACCCACCAACGTCGTCATCGCGACGCGTTCGCGACG 630  
 QY 94 AlaGlyPheCyLeuGlyHisAlaSerCyArgProGlyValGlyValIleAlaProGly 113  
 DB 629 CTC---TTCTGCTGGAGCAGCATCGTGTCCACTGT-GCCGCGGATGTCGCCCGGCG 574  
 QY 114 ThrProSerGlnAnThrGlnCysGlnProCySarProGlyThrPheSerAlaSerSer 133

DB 573 ACCCACTCCAGAAACAGCAGTCGACCGCTGCCCCCNAGGACCTTCTCAGCAGCAAGC 514  
 QY 134 SerSerSerGlyGlnCysGlnProHisArgAsnCyThrAlaLeuGlyLeuAlaLeuAsn 153  
 DB 513 TCCAGCTCAAGAGAGTGCACGCCCCACCGCACTGCACGCGCCCTGGGCGCTTCAAT 454  
 QY 154 ValProGlySerSerSerHisAspThrLeuCyThrSerCyThrGlyPheProLeuSer 173  
 DB 453 GTGCCAGGCTCTTCTTCCCATGTACACCTGTGCACCAAGCTGACTGCTTCCCCCTCAGC 394  
 QY 174 ThrArgValProGlyAlaGlyGlnCysGlyValArgAlaValIleAspPheValAlaPheGln 193  
 DB 393 ACCAGGGTACCAAGAGCTGAGGTGTGAGCGTGCCTCATCGCTTGTGGCTTTCAG 334  
 QY 194 AspTlIeserTlIeysArgLeuGlnArgLeuGlnAlaLeuGlnAlaProGlyGlyTyr 213  
 DB 333 GACATCTCCATCAAGAGGCTGCAGCGCTGCTCAGGCCCTCGAGGCCCGGAGGGCTGG 274  
 QY 214 GlyProThrProArgAlaGlyArgAlaAlaLeuGlnLeuLys-LeuArgArgArgLeuTh 233  
 DB 273 GTTCCGACACCAAGGCGGCGCGCGCTTGCAGCTGAACCTTGCTGCGGCTCAC 214  
 QY 233 rgjLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuGlnAlaLeuArgVa 253  
 DB 213 GGAGCTCTCGGGGCGCAGACGCGGCGCTGTGTGCTGCGCTGCTGACGCGCGCT 154  
 QY 253 lAlaArgMetProGlyLeuGlnArgSerValArgGlyArgPheLeuProValHis 271  
 DB 153 GGCGAGAGATCCCGGGCTGAGCGAGCGTCGTGAGCGCTTCTCCCTGTGCAC 99

RESULT 12  
 B1838357 588 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603083306F1 NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5222545 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1838357  
 VERSION B1838357.1 GI:15949907  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 588)  
 AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 http://image.liml.gov  
 Plate: LHM1559 row: 1 column: 02  
 High quality sequence stop: 588.

FEATURES  
 source  
 1.588  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:5222545"  
 /clone\_lib="NIH\_MGC\_120"  
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 /note="Organ: pooled pancreas and spleen; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of spleen and pancreas from 28 yo  
 male. Library is oligo-dT primed and directionally cloned  
 (EcoRV site is destroyed upon cloning). Average insert  
 size 1.5 kb, insert size range 1-2.5 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 025. Note: this is a NIH\_MGC Library."

BASE COUNT 97 a 224 c 171 g 95 t 1 others

ORIGIN

Alignment Scores: 7.6e-61 Length: 588

Pred. No.: 836.00 Matches: 145

Score: 97.97% Conservative: 0

Percent Similarity: 97.97% Mismatches: 3

Best Local Similarity: 97.97% Indels: 0

Query Match: 56.07% Gaps: 0

DB: 13

US-09-936-024-1 (1-271) x BI838357 (1-588)

QY 34 ArgArgAspSerProThrThrCysGlyProCysProProArgHisThrGlnPheTrp 53

Db 1 CGCCGAGACAGCCAGCAGTGTGGCCGTGTCCACCGCCACATACACGAGTTCTGG 60

QY 54 AsnTyrLeuGluArgCysArgTyrCysAsnValLeuCysGlyGluArgGluGluAla 73

Db 61 AACTACCTGGAGCGCTGCCGCTACTGCAAGCTCTCTGCGGGAGCGGTGAGGAGGCA 120

QY 74 ArgAlaCysHisAlaThrHisAsnArgAlaCysArgCysArgThrGlyPheAlaHis 93

Db 121 CGGGCTTGGCAGCCACCCACACCGCGCTGCGCTGCCGACCGCGCTTCTTCGCGCAC 180

QY 94 AlaGlyPheCysLeuGluHisAlaSerCysProProGlyAlaGlyValIleAlaProGly 113

Db 181 GCTGGTTCTTCTGGAGCAGCATCTGTCCACTGCTGCCGCGTGAATGCCCGGGC 240

QY 114 ThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAlaSer 133

Db 241 ACCCCAGCCAGAACACGCGAGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAG 300

QY 134 SerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAla 153

Db 301 TCCAGCTCAGAGCAGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAG 360

QY 154 ValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPheProLeu 173

Db 361 GTGCCAGCTCTTCTCTCCATGACAGCTGTGCACAGCTGCACAGCTGCACAGCTGC 420

QY 174 ThrArgValProGlyAlaGluGlu 181

Db 421 ACCANGGTACCGGTGAGCCAGAG 444

RESULT 13

AW262121/c

LOCUS

DEFINITION

qx311404.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2752231 3', similar to TR:095407 DECOY RECEPTOR 3. ;contains TAR1.b1

TAR1 repetitive element ;, mRNA sequence.

AW262121

VERSION

AW262121.1 GI:6638937

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

TITLE

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgaps-remail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found

Seq primer: -40UP from Gibco

High quality sequence stop: 410.

Location/Qualifiers

1. 600

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2752231"

/clone\_lib="NCI CGAP Lu28"

/tissue\_type="two pooled squamous cell carcinomas"

/lab\_host="DH10B"

/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."

BASE COUNT 120 a 177 c 199 g 102 t 2 others

ORIGIN

Alignment Scores: 6.77e-59 Length: 600

Pred. No.: 813.00 Matches: 156

Score: 98.12% Conservative: 1

Percent Similarity: 97.50% Mismatches: 3

Best Local Similarity: 54.53% Indels: 0

Query Match: 10 Gaps: 0

DB:

US-09-936-024-1 (1-271) x AW262121 (1-600)

QY 112 ProGlyThrProSerGlnAsnThrGlnCysGlnProCysProProGlyThrPheSerAla 131

Db 600 CCGGGCAGCCAGCCAGAACACGCGAGTGCAGCGTGCAGCGTGCAGCGTGCAGCC 541

QY 132 SerSerSerSerSerGluGlnCysGlnProHisArgAsnCysThrAlaLeuGlyLeuAla 151

Db 540 AGCAGCTCCAGCTCAGAGCAGTGCAGCGTGCAGCGTGCAGCGTGCAGCGTGCAG 481

QY 152 LeuAsnValProGlySerSerSerHisAspThrLeuCysThrSerCysThrGlyPhePro 171

Db 480 CTCAATGTGCAGGCTTCTCTCCATGACACCCCTGTCAGCAGCTGCAGCTGCAGCT 421

QY 172 LeuSerThrArgValProGlyAlaGluGluCysGluArgAlaValIleAspPheValAla 191

Db 420 CTCAGCAGCAGGGTACAGAGCTGAGGAGTGTGAGCGTGCAGCGTGCAGCTTGTGGCT 361

QY 192 PheGlnAspIleSerIleLysArgLeuGlnArgLeuGlnAlaLeuGluAlaProGlu 211

Db 360 TTCAGGACATCTCCATCAAGAGCTGCAGCGCTGCAGCGCTGCAGCGCTGCAGCG 301

QY 212 GlyTrpGlyProThrProArgAlaGlyArgAlaLeuGlnLeuLysLeuArgArgArg 231

Db 300 GGCTGGGTCCGACACCAAGGGCGGCGCGCGCTTGCAGCTGAAGCTGCAGCTGCAGCG 241

QY 232 LeuThrGluLeuLeuGlyAlaGlnAspGlyAlaLeuLeuValArgLeuGlnAlaLeu 251

Db 240 CTCAGCAGGCTCTTGGGGCGCAGGACGGGGCGCTGCTGGTGGCTGCTGCAGGCGCTG 181

QY 252 ArgValAlaArgMetProGlyLeuGluArgSerValArgGluArgPheLeuProValHis 271

Db 180 CGCGTGGCCAGAGTCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTTCCCTGTGCAC 121

RESULT 14

BM767088

LOCUS

DEFINITION

K-EST0049137 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-4-D01 5', mRNA sequence.

BM767088

ACCESSION

BM767088

VERSION

BM767088.1 GI:19096703

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



REFERENCE 1 (bases 1 to 605)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)  
 COMMENT Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 4 row: D column: 01  
 High quality sequence stop: 605.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="S1SNUS52-4-D01"  
 /clone\_11b="S1SNUS52"  
 /sex="F"  
 /tissue\_type="Ascites"  
 /cell\_type="Lymphoblast-like"  
 /cell\_line="SNU-5"  
 /lab\_host="Top10F"  
 /note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI; Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dt)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F with electroporation method."

BASE COUNT 87 a 221 c 203 g 94 t

ORIGIN

Alignment Scores:  
 Pred. No.: 3.32e-57 Length: 605  
 Score: 793.00 Matches: 135  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 53.19% Indels: 0  
 DB: 14 Gaps: 0

US-09-936-024-1 (1-271) x BM767088 (1-605)

Qy 1 ValAlaGluThrProCysProGlyThrPheValGlnArgLeuValCys 20  
 Db 201 GTGGCAAGAACACCCACTTACCTGGCGGACGACAGACGGGAGCGGCTGTGTGT 260  
 Qy 21 AlaGlnCysProGlyThrPheValGlnArgProCysArgGAspSerProThrThr 40

Db 261 GCCCAGTGGCCCCCAGGACCTTTGTGCACGGCCGCGCCGAGACACCCACGACG 320  
 Qy 41 CysGlyProCysProProAaGlnsTyrThrGlnPheThrPantTyrLeuGluArgCysArg 60  
 Db 321 TGTGGCCCGTGTCCACCGCCGACCTACACGAGTTCTGGAACTACCTGGAGCCCTGGCGC 380  
 Qy 61 TyrCysAsnValLeuGlyGlyGluArgGluGluGluAlaArgAlaCysHisAlaThrHis 80  
 Db 381 TACTGCACCTCTCTCTCGGGAGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440  
 Qy 441 AACCGCGCTCGCGCTGCCGACCGGCTTCTCGCGACCGCTGTTCTGTCGAGAC 500  
 Qy 101 AlAserCysProProGlyAlaGlyValIleAlaProGlyThrProserGlnAsnThrGln 120  
 Db 501 GCATCGTGTCCACCTGTGTGGCGGTGATTGCCCGGCGACCCCGACGAAACACGACG 560  
 Qy 121 CysGlnProCysProProGlyThrPheSerAlaSerSerSerSer 135  
 Db 561 TGCACGCCGTGCCCCCGACGACCTTCTCAGCAGCAGTTCACG 605

RESULT 15  
 BM767418 605 bp mRNA linear EST 04-MAR-2002  
 LOCUS BM767418  
 DEFINITION K-EST0049884 S1SNUS52 Homo sapiens cDNA clone S1SNUS52-5-B04 5', mRNA sequence.  
 ACCESSION BM767418  
 VERSION BM767418.1 GI:19097033  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 605)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)  
 COMMENT Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 5 row: B column: 04  
 High quality sequence stop: 605.  
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 /sex="F"  
 /tissue\_type="Ascites"  
 /cell\_type="Lymphoblast-like"  
 /cell\_line="SNU-5"  
 /lab\_host="Top10F"  
 /note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI; Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(drf)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10F' with electroporation method."

BASE COUNT 87 a 221 c 203 g 94 t  
ORIGIN

Alignment Scores:  
Pred. No.: 3,32e-57 Length: 605  
Score: 793.00 Matches: 135  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 53.19% Indels: 0  
DB: 14 Gaps: 0

US-09-936-024-1 (1-271) x BM767418 (1-605)

Qy	1	ValAlaGluThrProThrTyrProTyrArgAspAlaGluThrGlyGluArgLeuValCys	20
Db	201	GTGGCAGAAACACCCACTACCCCTGGCGGACGCAGACAGAGGAGCGCGTGGTGT	260
Qy	21	AlaGlnCysProProGlyThrPheValGlnArgProCysArgArgAspSerProThrThr	40
Db	261	GCCCAGTGCCCCCAGGACACCTTTGTGAGCGCGCGTGGCGGAGACAGCCCCCAGCG	320
Qy	41	CysGlyProCysProProArgHisTyrThrGlnPheTrpAsnTyrLeuGluArgCysArg	60
Db	321	TGTGGCCCGTGTCCACCGCGCCACTACACGAGTTCTGGAACTACCTGGAGCGGTGCCG	380
Qy	61	TyrCysAsnValLeuCysGlyGluArgGluGluAlaAlaArgAlaCysHisAlaThrHis	80
Db	381	TACTGCAACGTCTCTCGGGGAGCGTGAGGAGGAGGAGCGGCTTGCCACGCCACCCAC	440
Qy	81	AsnArgAlaCysArgCysArgThrGlyPhePheAlaHisAlaGlyPheCysLeuGluHis	100
Db	441	AACCGCGCTGCCCGCTGCCCGACCGGCTTTTCGCGCACGCTGGTTTCTGCTTGGAGC	500
Qy	101	AlaSerCysProProGlyAlaGlyValIleAlaProGlyThrProSerGlnAsnThrGln	120
Db	501	GCATCGTGTCCACTGGTGGCGGCGTGATTGCCCGGGCACCCCGCCAGCCAGACGCG	560
Qy	121	CysGlnProCysProProGlyThrPheSerAlaSerSerSerSer	135
Db	561	TGCCAGCGGTGCCCGCCCGGAGCACCTTCTCAGCCAGCAGTTCAGC	605

Search completed: January 6, 2003, 12:04:15  
Job time : 1972 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 6, 2003, 11:15:33 ; Search time 37 Seconds  
(without alignments)  
704.120 Million cell updates/sec

Title: US-09-936-024-1

Perfect score: 1491

Sequence: 1 VAETPTYPWRDAETGERLYC.....RVARMFGLERYVERFLPVH 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340.5	22.8	461	1 A35356	tumor necrosis fac
2	333.5	22.4	459	2 I48854	tumor murine tumour
3	332.5	22.3	474	2 B38634	tumor necrosis fac
4	299.5	20.1	435	2 I54182	tumor necrosis fac
5	289	19.4	651	2 JC7705	death receptor-6 -
6	260	17.4	348	2 T28623	hypothetical prote
7	260	17.4	349	2 D72175	CD2R protein - vari
8	260	17.4	349	2 D36858	gene G4R protein -
9	234.5	15.7	325	2 B43692	T2 protein - rabbi
10	215.5	14.5	277	2 I37552	OX40 homolog - hum
11	211.5	14.2	271	2 I21783	OX40 antigen precu
12	211	14.2	277	2 A60773	B-cell activation
13	210.5	14.1	336	1 GQVZML	T2 protein - myxom
14	203	13.6	305	2 A46476	B cell-associated
15	194.5	13.0	272	2 I48700	gene OX40 protein
16	185	12.4	256	2 B32393	T-cell antigen 4-1
17	182	12.2	595	2 A42086	CD30 antigen precu
18	174	11.7	255	2 I38426	lymphocyte activat
19	171.5	11.5	416	1 JN0006	nerve growth facto
20	168	11.3	435	1 A26431	nerve growth facto
21	158	10.6	427	1 GQHUN	nerve growth facto
22	155.5	10.4	337	1 A46484	apoptosis-mediatin
23	148.5	10.0	1574	2 T13954	MEGF6 protein - ra
24	148	9.9	250	1 A49053	CD27 antigen precu
25	147.5	9.9	5376	2 T42215	zonahesin - mouse
26	146.5	9.8	260	1 A46517	CD27 antigen precu
27	145	9.7	335	2 A40036	apoptosis-mediatin
28	143	9.6	1620	2 T27283	hypothetical prote
29	140	9.4	314	2 I37383	FAS soluble protei

30	137.5	9.2	324	2 UC2395	Fas antigen precu
31	135.5	9.1	1299	2 T42251	furin (EC 3.4.21.7
32	135	9.1	2321	2 S78549	notch3 protein - h
33	130.5	8.8	454	1 GOMST1	tumor necrosis fac
34	128.5	8.6	3635	2 T10053	lamnin alpha 5 ch
35	127	8.5	1192	2 S69000	lamnin gamma 2 ch
36	125.5	8.4	1548	2 S34583	serine proteinase
37	124.5	8.4	1713	2 A55347	adhesive ligand ep
38	123.5	8.3	455	1 GQHUT1	tumor necrosis fac
39	123.5	8.3	493	2 JC5486	membrane glycoprot
40	122.5	8.2	2824	2 T23759	hypothetical prote
41	121	8.1	3106	1 S53868	lamnin alpha-2 ch
42	120	8.0	1609	1 MMHUB2	lamnin gamma-1 ch
43	119.5	8.0	3084	1 MMMSA	lamnin alpha-1 ch
44	118.5	7.9	461	1 GQRTT1	tumor necrosis fac
45	118.5	7.9	1680	2 A43434	furin (EC 3.4.21.7

## ALIGNMENTS

RESULT 1  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N:Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext change 08-Dec-2000  
C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  
Science 248, 1019-1023, 1990  
A>Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
A:Reference number: A35356; WUID:90260639; PMID:2160731  
A:Accession: A35356  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-461 <SMI>  
A:Cross-references: GB:M32315; NID:9189185; PIDN:AAA5929.1; PID:9189186  
R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,  
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990  
A>Title: A second tumor necrosis factor receptor gene product can shed a naturally occur  
A:Reference number: A36475; WUID:91045991; PMID:2172583  
A:Accession: A36475  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-195 'R', 197-461 <KOH>  
A:Cross-references: GB:M55994; GB:M8549; NID:9339757; PIDN:AAA36755.1; PID:9339758  
R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.;  
Cytokine 2, 231-237, 1990  
A>Title: Two human TNF receptors have similar extracellular, but distinct intracellular,  
A:Reference number: A48416; WUID:91370690; PMID:1966549  
A:Accession: A48416  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-461 <DEM>  
A:Cross-references: GB:S63368; NID:9235648; PIDN:AA19824.1; PID:9235649  
A>Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)  
R:Heiler, R.A.; Song, K.; Onach, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990  
A>Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat  
A:Reference number: A36007; WUID:90349572; PMID:2166946  
A:Accession: A36007  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 116-140 'P', 142-195 'R', 197-362 'T', 364-461 <HEI>  
A:Cross-references: GB:M35857; NID:9339751; PIDN:AAA3262.1; PID:9339752  
R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.  
J. Biol. Chem. 265, 20131-20138, 1990  
A>Title: Purification and partial amino acid sequence analysis of two distinct tumor nec  
A:Reference number: A23666; WUID:91056048; PMID:2173596  
A:Accession: A23666  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 23-40/65-69/136-141/300-306 <LOE>

A;Residues: 1-459 <RES>  
A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831  
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 22.4%; Score 333.5; DB 2; Length 459;  
Best Local Similarity 29.7%; Pred. No. 6.3e-16;  
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

QY 17 RLVAQCPTGTVQPCRRDSTTCGPCHRYTDFMNYLCRCYNVLCGEREERARAC 76  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 37 QMCAKCPGVQIVKHFNKTSTVDCADCEASMYTVWNNQFTCLSCSSCSSTDQVEFRAC 96  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 77 HATHNRACRRTGFF-----AHAGF---CLEHASCPPGAGVIAPGTSPQNTOCPCPGTF 129  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 97 TKQNVRVACEAGRYCALKTHSGSCRCQWRLSKCGPFGVASSRAPNGNVLCACAPGTF 156  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 130 SASSSSSECOQHRCNTALGLANVPSSSHDTLCT----SCTGFPLSTRVPGARECERA 185  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 157 SDTTSDDVCRRHCISILA----IPGNASTDAVCAPESTILSAIPRTLVSQSPEPTRSQ 212  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 186 VIDFAVFQDISIKRLQLLOALEAFEGGTPP-----BAGRAALQLKLRRRLTELLGAQD 240  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 213 PLD-----QPGPSQPSILTSU-----GSTPIIQSKGGISLPGLIVGVTSL----- 257  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 241 GALLVRELLOAL----RVARMPLGLERSVREFLP 269  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db 258 GLJMLGLVNCFLVQRKKPKSLQRDAKVHPV 290  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 3  
B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Jul-1999  
C;Accession: B38634; A40254; S54816  
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
A;Reference number: A38634; MUID:91187885; PMID:1849278  
A;Accession: B38634  
A;Molecule type: mRNA  
A;Residues: 1-474 <LEW>  
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Je  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors fo  
A;Reference number: A40254; MUID:91246168; PMID:1645445  
A;Accession: A40254  
A;Molecule type: mRNA  
A;Residues: 1-474 <GOO>  
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828  
R;Kisnerghis, M.; Fellows, R.; Feldmann, M.; Chernaajovsky, Y.  
submitted to the EMBL Data Library, May 1995  
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.  
A;Reference number: S54816  
A;Accession: S54816  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-22 <KIS>  
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044  
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C;Keywords: cytokine receptor; transmembrane protein  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F;40-70/Domain: NGF receptor repeat homology <NG1>  
F;79-120/Domain: NGF receptor repeat homology <NG2>  
F;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 22.3%; Score 332.5; DB 2; Length 474;  
Best Local Similarity 29.7%; Pred. No. 7.7e-18;  
Matches 81; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

QY 17 RLVCACPPGTFVQRPDRDPTTCGPPCPRHAYTOFNNYLERCRYCNVLGEEBEARAC 76  
A:Accession: J07705  
A:Molecule type: mRNA  
A:Residues: 1-651 <BRI>  
A:Cross-references: GB:AF349908  
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs  
to the TNF receptor superfamily, class I, member 1, and is involved in the TNF signaling  
cascade.  
C:Gene: dr-6  
A:Gene: dr-6  
C:Keywords: ovary  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:32-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>  
F:332-350/Domain: transmembrane #status predicted <TM>  
F:410-475/Domain: death domain #status predicted <DED>  
F:551-651/Region: conserved cytoplasmic #status predicted

Db 112 TKQNNVCAACEARVCAKLTGSHGSCRCMRLSKCGPFGVASSRAPNGVNLCAACAGPT 171  
QY 130 SASSSSEOCQPHNCTALGLALNVPGSSSHDILCT-----SCGFPPLSTVPGABECERA 185  
Db 172 SDTSTSDVCRPHRICSLA-----IPGNASTDVCADBPSTLSAIFPTLVYSGPEPTRSQ 227  
QY 186 VIDFVAFODISIRLOLQALBAPBEGMGPTP-----RAGRAALQTLRRRLTELLGAOD 240  
Db 228 PLD-----QEGPFGQTSILTSL-----GSTPIEOSTKGISLPLGLIVGVSIL----- 272

QY 241 GALLVRLLOAL-----RVARNPGLERSVREFFLP 269  
Db 273 GLIMLGIVNCIILVQRKKKPSCLQRDAKVPHPV 305

## RESULT 4

154182  
tumor necrosis factor receptor 2-related protein - human  
C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000  
C:Accession: 154182  
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Maeynen, P.  
Genomics 16, 214-218, 1993  
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen  
A:Reference number: 154182; MUID:93252381; PMID:8486360  
A:Accession: 154182  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-435 <RES>  
A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762  
C:Gene: GDB:L7BR  
A:Gene: GDB:L7BR  
A:Cross-references: GDB:1230195; OMIM:600979  
A:Map position: 12p13.3-12p13.1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 20.1%; Score 299.5; DB 2; Length 435;  
Best Local Similarity 32.0%; Pred. No. 2,2e-15;  
Matches 74; Conservative 27; Mismatches 101; Indels 29; Gaps 9;

QY 13 ETGERLVCAOCPGTFVQRPDRDPTTCGPPCPRHAYTOFNNYL---ERCRCNVLCGER 69  
Db 52 EPQHRIICSCRPGETVYSAKCSRIADTVCAICAEINSYEHNNYLTICQLCRPCDPVWG-- 109  
QY 70 EEARACHATHNRACRCRTGFPAHAGFCLF--H---ASCPPGA-GVIAEGTESQNTQCC 122  
Db 110 LLEBIAPCTSKRKTCQRCQPGWFC--AAWALECTHCELLSDCPGEABELKKEVGKGNHCV 168  
QY 123 PCPPGTSASSSSEOCQPHNCTALGLALNVPGSSSHDILCTSCGTPSPILSTRVGAEEC 182  
Db 169 PCAGHFGONTSSSARCAQPHRCENQGLVEAPAFIAGSDITTKAPLE-PLPPEKSGTMLM 227

QY 183 ERAVIDFVAFODIS-----IKRLQRLQALBAPBEGMGPTPRAG 220  
Db 228 LAVLLPLAFLLATVPSCIWKSHPLSLCRKLGSLLK--RRQGGSGPRVAG 276

## RESULT 5

J07705  
death receptor-6 - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: J07705  
R:Brigham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.  
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001  
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.  
A:Reference number: J07705; MUID:21308433; PMID:11414698

A:Accession: J07705  
A:Molecule type: mRNA  
A:Residues: 1-651 <BRI>  
A:Cross-references: GB:AF349908  
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs  
to the TNF receptor superfamily, class I, member 1, and is involved in the TNF signaling  
cascade.  
C:Gene: dr-6  
A:Gene: dr-6  
C:Keywords: ovary  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:32-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>  
F:332-350/Domain: transmembrane #status predicted <TM>  
F:410-475/Domain: death domain #status predicted <DED>  
F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 19.4%; Score 289; DB 2; Length 651;  
Best Local Similarity 33.5%; Pred. No. 2e-14;  
Matches 54; Conservative 27; Mismatches 80; Indels 0; Gaps 0;

QY 11 DAETGERLVCAOCPGTFVQRPDRDPTTCGPPCPRHAYTOFNNYLERCRYCNVLGGER 70  
Db 43 DRATNGELICDKCPATVYSKHTKSTLRCSPCPDGTFKHENGIERCHPCKRCELP 102  
QY 71 EEARACHATHNRACRCRTGFPAHAGFCLFHAASCPGAGVIAPTSPQNTQCCPPTGFS 130  
Db 103 IEKHTCTALTRDCTCTGTFQINDCVPTVCVPGVGVKKGTEDEVRCKPCLRGTF 162

QY 131 ASSSSSEOCQPHNCTALGLALNVPGSSSHDILCTSCGTP 171  
Db 163 DVPSVWCKCTYDCEGKNVNVVVKFKESDNVCSAPSILP 203

## RESULT 6

T28623  
hypothetical protein G2R - variola major virus  
C:Species: variola major virus  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T28623  
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utteback, T.R.; Knight, J.C.; Aubin,  
Nature 386, 748-751, 1993  
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus  
A:Reference number: Z20488; MUID:94088747; PMID:8264798  
A:Accession: T28623  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-348 <NAS>  
A:Cross-references: EMBL:122579; NID:9623595; PIDN:AAA60933.1; PID:g439102  
A:Experimental source: strain Bangladesh 1975  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 348;  
Best Local Similarity 32.2%; Pred. No. 1.7e-12;  
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWRDAE-TGERLVCAOCPGTFVQRPDRDPTTCGPPCPRHAYTOFNNYLERCRYCN 63  
Db 27 PNGKCKDTEKRNHLCISCPETVYASRLCDSTNTQCTCGSGTFSRNHPLACISCN 86  
QY 64 VLGEREEARACHATHNRACRCRTGFF-----AHAGFCLHAASCPGAGVIAPTSPQ 117  
Db 87 GRGNSNQVETRSCNTTHNRICECSPGYCYLLKSSGCKACVSGTKGIGYV-SGHTSVG 145

QY 118 NTQCCPPTGTFASSSSSQCPHRCNTALGLALNVPGSSSHDILCTSCGTFPLSTRVP 177  
Db 146 DVICSPCGFTSHVTSADKCEVPNNTPNYIDVELTLYPVADTSCRTTYYTGLSESL 205

QY 178 GAE 180  
Db 206 TSE 208

## RESULT 7

D72175

G2R protein - variola minor virus (strain Garcia-1966)  
C:Species: variola minor virus  
C:Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000  
C:Accession: D72175  
R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Massung, R.F.; Lopau  
submitted to GenBank, March 1998  
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor  
A:Reference number: A72150  
A:Accession: D72175  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <SHC>  
A:Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759  
A:Experimental source: strain Garcia-1966  
C:Genetics:  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 349;  
Best Local Similarity 32.2%; Pred. No. 1.7e-12;  
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWRDAE-TGERLVCAQCPGTFVQPCRRDSTTCGPPRHYTFQWNYLRCRYCN 63  
DB 28 PNGCKDTEYKRNLCCLSCPPGTYASRLCDSTNTQCTPCGSGTFTSRNHLPACLSCN 87

QY 64 VLGEREEERACHATHNACRRTGFF-----AHAGFLEHASCPGAGVIAPGTPSQ 117  
DB 88 GRCNSNQVETRSCNTTHNRICECPGYCLLKGSSGCKACVQTKCGIGYGV-SGHTSVG 146

QY 118 NTOCQCPGPTFSASSSSSEQPHRNCCTALGLALNVPSSSHDTLCTCTGPPPLSTRVP 177  
DB 147 DVICSPCGFTYVTSSTDKCEPVNNTFNIDVEITLIPVNDTSCRTTTGLSESIL 206

QY 178 GAE 180  
DB 207 TSE 209

RESULT 8  
D36858  
Gene G4R protein - variola virus  
N:Alternate names: B28R protein (COP)  
C:Species: variola virus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 23-Mar-2001  
C:Accession: D36858; S46888; S32385; S35987  
R:Blinov, V.M.  
submitted to GenBank, November 1992  
A:Reference number: A36859  
A:Accession: D36858  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <BLI>  
A:Cross-references: GB:X69198; NID:G456758; PIDN:CAA49137.1; PID:G457087  
A:Experimental source: strain India-1967, ssp. major, isolate Ind3  
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Fro  
submitted to the EMBL data Library, April 1992  
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P  
A:Reference number: S46868  
A:Accession: S46888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <COL>  
A:Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449  
A:Experimental source: strain India-1967, isolate Ind3  
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.  
FEBS Lett. 319, 80-83, 1993  
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective  
A:Reference number: S32385; MUID:93202281; PMID:8384129  
A:Accession: S32385  
A:Molecule type: DNA  
A:Residues: 31-168 <SHC>  
A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major  
C:Genetics:  
A:Gene: G4R  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
F:32-66/Domain: NGF receptor repeat homology <NGP>  
F:68-109/Domain: NGF receptor repeat homology <NGP>  
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 17.4%; Score 260; DB 2; Length 349;  
Best Local Similarity 32.2%; Pred. No. 1.7e-12;  
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYPWRDAE-TGERLVCAQCPGTFVQPCRRDSTTCGPPRHYTFQWNYLRCRYCN 63  
DB 28 PNGCKDTEYKRNLCCLSCPPGTYASRLCDSTNTQCTPCGSGTFTSRNHLPACLSCN 87

QY 64 VLGEREEERACHATHNACRRTGFF-----AHAGFLEHASCPGAGVIAPGTPSQ 117  
DB 88 GRCNSNQVETRSCNTTHNRICECPGYCLLKGSSGCKACVQTKCGIGYGV-SGHTSVG 146

QY 118 NTOCQCPGPTFSASSSSSEQPHRNCCTALGLALNVPSSSHDTLCTCTGPPPLSTRVP 177  
DB 147 DVICSPCGFTYVTSSTDKCEPVNNTFNIDVEITLIPVNDTSCRTTTGLSESIL 206

QY 178 GAE 180  
DB 207 TSE 209

RESULT 9  
B43692  
T2 protein - rabbit fibroma virus  
C:Species: rabbit fibroma virus, Shope fibroma virus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: B43692  
R:Upton, C.; DeLange, A.M.; McFadden, G.  
Virology 160, 20-30, 1987  
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric  
A:Reference number: A43692; MUID:87321103; PMID:2820128  
A:Accession: B43692  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-325 <UPT>  
A:Cross-references: GB:M17433  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
F:64-105/Domain: NGF receptor repeat homology <NG2>  
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 15.7%; Score 234.5; DB 2; Length 325;  
Best Local Similarity 32.9%; Pred. No. 1.4e-10;  
Matches 52; Conservative 19; Mismatches 76; Indels 11; Gaps 3;

QY 18 LVCAQCPGPTFVQPCRRDSTTCGPPRHYTFQWNYLRCRYCNVLCGEREEERACH 77  
DB 38 LCCASCHPGFYASRLCGPSNTVCSCEGDTFTASTNHAPACVSCGCTGHLSESQPCD 97

QY 78 ATHNACRRTGFFA-----HAGFLEHASCPGAGVIAPGTPSQNTQCPCPGTFFSA 131  
DB 98 RTHDRVCSGTGNYCLLKGQNGCRICAPQTKCPAGYGV-SGHTRAGDTLCEKCPPTYS 156

QY 132 SSSSSFQCPHRNCTALGLALNVPSSSHDTLCTCTG 169  
DB 157 SUSPTERCSTFNYSVGFNL----YPVNETSCTTTAG 190

RESULT 10  
I37552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fona  
Eur. J. Immunol. 24, 677-683, 1994

A>Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
A:Reference number: 137552; MUID:94170844; PMID:7510240  
A:Accession: 137552  
A>Status: preliminary; translated from GB/EMBL/DBD  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA5376.1; PID:9472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 14.2%; Score 215.5; DB 2; Length 277;  
Best Local Similarity 27.0%; Pred. No. 3.2e-09;  
Matches 72; Conservative 22; Mismatches 104; Indels 69; Gaps 11;

QY 6 TYPMRDAETGERLVCAQCPPTGFVQRPDRSDPTTCGCPPEPRHYTOPWNY--LERCRVCN 63  
DB 35 TYPSNDR-----CCHCRPRGNGVNSRCSQNTVCRPCGCGFNDVVSSEKPCPCWCN 88  
QY 64 VLGEREERARACHATNRACRCRGTGFPAHAGFLEHASCPGAGVTAAGTPTGQNTCCQ 123  
DB 89 LRSQ--SERKQLCTATQDTVCRCRAG-----TQPLDSYKFG-----VDCAP 127  
QY 124 CPPTGSASSSSSECOQPHNCTALGLALVNPSSSHDTICTS---CTGFPLSTRVGCAG 180  
DB 128 CPFGHF--SPGNDQACKPMWNTCTLAGKHTLQPAISSSDAICEDRDPATQPOETQGPAP 185  
QY 181 ECRRAVIDFVAQDISIKRLQLALEAPEGW-----GTPPR-----AGRAALQLRLR 230  
DB 186 PL-----TQPRFANPRTSGSGSTRVPEVPGRAVAAILGLG 222  
QY 231 RLTELLGAODGALLVRLQLARVAMP 257  
DB 223 LVVGLGLPL--AIIALLYLRLRQRLP 247

RESULT 11  
S12783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homology  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Maillet, S.; Fossuem, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990  
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes  
A:Reference number: S12783; MUID:90214614; PMID:2157591  
A:Accession: S12783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA4897.1; PID:957831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <MAT>  
F:211-235/Domain: transmembrane #status predicted <MAT>

Query Match 14.2%; Score 211.5; DB 2; Length 271;  
Best Local Similarity 31.5%; Pred. No. 6.4e-09;  
Matches 53; Conservative 18; Mismatches 54; Indels 43; Gaps 8;

QY 6 TYPMRDAETGERLVCAQCPPTGFVQRPDRSDPTTCGCPPEPRHYTOPWNY--LERCRVCN 63  
DB 30 TYD-----SGHK--CCRCQCGHGVNSRCDHTRDVCHPCBEGFVNEAVNVDTCQCTQCN 83  
QY 64 VLGEREERARACHATNRACRCRGTGFPAHAGFLEHASCPGAGVTAAGT-PSQNT--- 119  
DB 84 HRSQ--SELKQNTPTEDTVCQCR-----PQTPRQDSHK 117  
QY 120 ---QCQCPPTGSASSSSSECOQPHNCTALGLALVNPSSSHDTLC 164  
DB 118 LGVDTCPCPFGHF--SPGSDQACKPMWNTCTLSGKQIHNPASNSLDIVC 163

RESULT 12

A60771  
B-cell activation protein CD40 precursor - human  
N:Alternate names: B-cell surface antigen Bp50  
C:Species: Homo sapiens (man)  
C>Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 21-Jul-2000  
C:Accession: S04460; A60771  
R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
EMBO J. 8, 1403-1410, 1989  
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
A:Reference number: S04460; MUID:89356608; PMID:2475341  
A:Accession: S04460  
A:Molecule type: mRNA  
A:Residues: 1-277 <STA>  
A:Cross-references: EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851  
R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nike, H.; Aspenstroem, P.; Perlmann, P.  
J. Immunol. 142, 562-567, 1989  
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
A:Reference number: A60771; MUID:89093941; PMID:2463309  
A:Accession: A60771  
A:Molecule type: protein  
A:Residues: 21-50 <BRA>  
A:Experimental source: Burkitt lymphoma cell line Raji  
C:Genetics: GDB:CD40  
A:Gene: GDB:CD40  
A:Cross-references: GDB:215268; OMIM:109535  
A:Map position: 20q12-20q13.2  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>  
F:21-193/Domain: extracellular #status predicted <EXT>  
F:194-215/Domain: transmembrane #status predicted <TM>  
F:216-277/Domain: intracellular #status predicted <CT>  
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.2%; Score 211; DB 2; Length 277;  
Best Local Similarity 30.5%; Pred. No. 7.1e-09;  
Matches 46; Conservative 21; Mismatches 76; Indels 8; Gaps 3;

QY 20 CAQCPPTGFVQRPDRSDPTTCGCPPEPRHYTOPWNYLER--RYCNVLGEREERARAC 76  
DB 38 CSIDCPQKIVSDCTEFTETECLPGCESEFLDPMNRETHCHQHKYCDPNLGLVQQGTS 97  
QY 77 HAHNNAACRCRGTGFPAH---GFCLEHASCPPGAGVTAAGTPTGQNTCCQCPPTGSASS 133  
DB 98 ET--DTITCTCEBGMHCTSEACSCVLRHSCSPGKQIATGVSDITCEPCVGFPSNV 155  
QY 134 SSSECOQPHNCTALGLALVNPSSSHDTLC 164  
DB 156 SAPEKCHPWTSCETKQLVQQAETNKTIVVC 186

RESULT 13  
GOVZML  
T2 protein - myxoma virus (strain Lausanne)  
C:Species: myxoma virus  
C>Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999  
C:Accession: A40566  
R:Updon, C.; Macen, J.L.; Schreiber, M.; Mcfadden, G.  
Virology 184, 370-382, 1991  
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor  
A:Reference number: A40566; MUID:91335768; PMID:1651597  
A:Accession: A40566  
A:Molecule type: DNA  
A:Residues: 1-326 <UPT>  
A:Cross-references: GB:M95181; GB:M37976; NID:9332309; PIDN:AAA46632.1; PID:9332310  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
C:Keywords: glycoprotein  
F:64-105/Domain: NGF receptor repeat homology <NG>  
F:106-147/Domain: NGF receptor repeat homology <NG3>  
F:166,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.1%; Score 210.5; DB 1; Length 326;

